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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:18:13 ; Search time 20.3912 Seconds
(without alignments)
2367.669 Million cell updates/sec

Title: US-09-783-931-2

Perfect score: 4153

Sequence: 1 MGRFLTLALLSALLCRQ.....YQSVYVISEKDECIATTEV 728

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4153	100.0	728	3	US-08-981-392-2
2	4153	100.0	728	4	US-09-908-322-2
3	4142.5	99.7	729	3	US-08-872-855-8
4	3495.5	84.2	721	3	US-08-981-392-5
5	3495.5	84.2	721	4	US-09-908-322-5
6	3494.5	84.1	723	3	US-09-068-740A-9
7	3494.5	84.1	723	4	US-09-423-753-27
8	3494.5	84.1	723	4	US-10-140-002-346
9	3491.5	84.1	721	3	US-08-872-855-7
10	3466.5	83.5	723	4	US-09-641-612-6
11	3445.5	83.0	702	3	US-09-068-740A-4
12	3375	81.3	720	3	US-08-872-855-4
13	3368	81.1	722	3	US-08-981-392-12
14	3346.5	80.6	713	3	US-09-908-322-12
15	3346.5	80.6	713	4	US-08-872-855-5
16	3061.5	73.7	717	3	US-08-872-855-9
17	2784	67.0	520	3	US-09-068-740A-3
18	2489	59.9	578	3	US-08-981-392-13
19	2489	59.9	578	4	US-09-908-322-13
20	1928	46.4	642	3	US-08-872-855-10
21	1897	45.7	685	3	US-08-872-855-2
22	1897	45.7	685	4	US-09-423-753-25
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24	1897	45.7	685	4	US-10-140-002-88
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34	1555.5	37.5	832	3	US-08-981-392-6
35	1555.5	37.5	832	4	US-09-908-322-6
36	1534.5	36.9	830	3	US-08-872-855-11
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38	1354	32.6	1218	3	US-08-611-729A-6
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41	1353	32.6	1208	4	US-09-199-865-1
42	1349	32.5	1219	3	US-08-882-046-5
43	1349	32.5	1219	4	US-09-566-047-5
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45	1348.5	32.5	1193	3	US-08-611-729A-10

ALIGNMENTS

RESULT 1
US-08-981-392-2
; Sequence 2, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henriquez, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-392-2

Query Match 100.0%; Score 4153; DB 3; Length 728;
Best Local Similarity 100.0%; Pred. No. 1.le-304;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 HHKPCNKGATCTNTGQSYTCSRCRPGYTGSSCBIEINECDANPCKNKGSGCTDLENSYSCT 360
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RESULT 2

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US-09-908-322-2
; Sequence 2, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
;             Henrique, Domingos Manuel Pinto
;             Lewis, Julian Hart
;             Artavanis-Tsakonas, Spyridon
;             Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
;                     VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-908-322-2

Query Match 100.0%; Score 4153; DB 4; Length 728;
Best Local Similarity 100.0%; Pred. No. 1.1e-304;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRFLLTLLSALLCQVDSGVFELKQBFVNKGLLSNRNCRGGGPGAGQQQC 60
Db 1 MGRFLLTLLSALLCQVDSGVFELKQBFVNKGLLSNRNCRGGGPGAGQQQC 60
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Db 61 DCKTFRVCLKHQASVSPPECTYGSATIPVLGANSFSPDGAGGADPAFSPNIRFPFG 120
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Db 421 CANGAACQVDLGNYSYICQCAQAGTGRHCDNDVDDCASFPFCVNGGTCQDGVNDYSCTCPPGY 480
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Db 541 EKYTEGQNSQFPWIAVCAGIILVLLGCAAVVCLVKVQRHHQPEACRSETETMNN 600
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Qy 721 ECIATEV 728
Db 721 ECIATEV 728
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US-08-872-855-8
; Sequence 8, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-8
Query Match 99.7%; Score 4142.5; DB 3; Length 729;
Best Local Similarity 99.9%; Pred. No. 6.5e-304;
Matches 728; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 1 MGGRLTLTALLSALLCRQVDGSGVFELKIQEFVNKKGLLSNRNCCRGCGPGAGQQQC 60
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Db 181 SYFVCDDEHYGEGSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
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Db 301 HHKPKCKNGATCTNTGQGSYTCSCRPGYTGSSECEIEINECDANPCKNGGSCDTLNSYSCT 360
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Db 361 CPPGFYGNKCELSAMTCADGFCFNGGRCCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420
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Db 421 CANGAQ-CVDLGNYSYICQCAQAGFTGRHCDNDVDDCASFPVCVNGGTCCDGVNDYSCTCPG 480
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Db 481 YNGKNCSTPVSRCHEHNPCHNGATCHEHSNRVYVCECARGYGGLNCQFLLPEPPQGPVIVDF 540
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Db 541 TEKYTEQNSQFPWIAVCAGIILVLLMLLGCALIVCVRLKVKQRHHQPEACRSETETMN 600
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Db 601 NLANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVDYVNLVHELKNEHSV 660
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Db 661 VKBEHGKCEAKCETVDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVVISBEK 720
Qy 720 DECIATEV 728
Db 721 DECIATEV 729
RESULT 4
US-08-981-392-5
; Sequence 5, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ancier, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-981-392-5

Query Match 84.2%; Score 3495.5; DB 3; Length 721;
Best Local Similarity 82.2%; Pred. No. 3.7e-255;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;
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Db 1 MQQRMILLVLSAVL--CQISCSGLFELRLQEFVNNKGLLGNMCCR---PGSLASLQR 55
QY 60 CDCKTFFRVLKHYQASVSPPECTYGSNAITPVLGANSFSPDGAGADPAFNPFRPF 119
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QY 240 QHGFCDKPGCKRCRVGQGRYQDECIRYPGCLHGTCQQPWCNCGQWGLFCNQDLNYC 299
Db 235 HHGYCDKPGCKRCRVGQGRYQDECIRYPGCLHGTCQQPWCNCGQWGLFCNQDLNYC 294
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Db 415 PCANGARCEDLGNYSYTCQCAQFTGRHDDNDVDCASFPVCNGGTCQDQGVNDYSCTCPPG 474
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Db 475 YGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCOPLLEPPQGPVVDVF 532
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QY 719 KDECIATEV 728
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RESULT 5
US-09-908-322-5
; Sequence 5, Application US/09908322

Patent No. 6783956
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Taakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
Query Match 84.2%; Score 3495.5; DB 4; Length 721;
Best Local Similarity 82.2%; Pred. No. 3.7e-255;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;
QY 1 MGRFLLTLLALLSALLCRCQVDGSGVFLKLOEFVNNKGLLSNRNCCRGPGG-AGQOO 59
Db 1 MQQRMILLVLSAVL--CQISCSGLFELRLQEFVNNKGLLGNMCCR---PGSLASLQR 55
QY 60 CDCKTFFRVLKHYQASVSPPECTYGSNAITPVLGANSFSPDGAGADPAFNPFRPF 119
Db 56 CECKTFFRVLKHYQASVSPPECTYGSNAITPVLGANSFSPDGAGADPAFNPFRPF 114
QY 120 GFTWPGTFSLLIEALHTDSDPDLTTENPERLISRLATQRLHLAGVSEWSDHSSGRTDLK 179
Db 115 GFTWPGTFSLLIEALHTDSDPDLTTENPERLISRLATQRLHLAGVSEWSDHSSGRTDLK 174
QY 180 YSYRFVCDHYHYGEGSCVFCRPRDRFHTCGERGEKVCNPGWKGYCTEPICLPGCDE 239
Db 175 YSYRFVCDHYHYGEGSCVFCRPRDRFHTCGERGEKVCNPGWKGYCTEPICLPGCDE 234
QY 240 QHGFCDKPGCKRCRVGQGRYQDECIRYPGCLHGTCQQPWCNCGQWGLFCNQDLNYC 299
Db 235 HHGYCDKPGCKRCRVGQGRYQDECIRYPGCLHGTCQQPWCNCGQWGLFCNQDLNYC 294
QY 300 THHKPCNKGCATCTNTGQSYTCSRGYTGSCRETEINECDANPCNKGSCDTLENSYSC 359
Db 295 THHKPCNKGCATCTNTGQSYTCSRGYTGSCRETEINECDANPCNKGSCDTLENSYSC 354


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Db 295 THHKPCNGATCTNTGQSYTCSRCRPGYTGNCCEIEVNECDANPCCKNGGSCDLENSYTC 354
Qy 360 TCPGFGYKNCELSAMTADGPCFNGRGCTONPDGYSRCPLGYSGFNCCKKIDYCSSS 419
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
355 SCPPGFGYKNCELSAMTADGPCFNGRGCAADNPDGGYICFCPVGYSGFNCCKKIDYCSN 414
Qy 420 PCANGAQCVDLGNYSYCOCQAGFTGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPG 479
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
415 PCANGARCEDLGNYSYCOCQAGFTGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPG 474
Qy 480 YNGKNCSTPVSRCBNPCHNGATCHERSNRYVCECARGYGGLNCOFLLPPEPQGPVVD 539
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
475 YIGKNCSTPVSRCBNPCHNGATCHERSNRYVCECARGYGGLNCOFLLPPEPQGPVVD 532
Qy 540 TEKTEGQNSOPPIAVCAGIILVLMMLLGGCAAVVCLVLRKVKQRRHHPQACRSETETMN 599
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
533 TEKTEGQNSOPPIAVCAGIILVLMMLLGGCAAVVCLVLRKVKQRRHHPQACRSETETMN 592
Qy 600 NLANCOREKDISISVIGATQIKNTNKKVDPHSD-NSDKNGYKVRYPVSDYNLVHELKNE 658
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
593 NLANCOREKDISISVIGATQIKNTNKKVDPHSD-NSDKNGYKVRYPVSDYNLVHELKNE 652
Qy 659 SVKEHKGCEAKCETYSDEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 718
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
653 SPKERSKCEAKCSNDSNDSVNSVHSK-RDSSERRRPDSAYSTSKDTKYQSVYVISE 711
Qy 719 KDECIITATEV 728
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
712 KDECIITATEV 721
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RESULT 6
US-09-068-740A-9
; Sequence 9, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-068-740A-9
```

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Query Match 84.1%; Score 3494.5; DB 3; Length 723;
Best Local Similarity 83.3%; Pred. No. 4.4e-255;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy 1 MGRFLTLTALLSALLCRCQVDSGVFELKQLQEFVNKGLLSNRNCCRGCGGPGGAGQOQC 60
Db 1 MGRSCALALAVLSALL--CQVSSGVFELKQLQEFVNKGLLSNRNCCR---GGAGPPPC 54
Qy 61 DCKTFFRVCLKHQYQASVSPPEPCTYGSATPVLGANSFSDVDPDAGGADPAFSPNIRPFG 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
55 ACRTFFRVCLKHQYQASVSPPEPCTYGSATPVLGANSFSDVDPDAGGADPAFSPNIRPFG 113
Qy 121 FTWPGTSLIEALHTDPSDDLTENPERLISRLATORHLAVGSEWSDLHSSGRTDLKY 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
114 FTWPGTSLIEALHTDPSDDLTENPERLISRLATORHLAVGSEWSDLHSSGRTDLKY 173
Qy 181 SYRFVCDHEHYGEGCSVFCRPRDRFGHTTCGERGEKVCNPGMKGYCTEPICLPGCDEQ 240
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Db 174 SYRFVCDHEHYGEGCSVFCRPRDRFGHTTCGERGEKVCNPGMKGYCTEPICLPGCDEQ 233
Qy 241 HGFCDKPEGECKRCRVGMQGRYCDCEIRYPCGLHGTCCQPMQCNCOBGWGLFCNODLNYCT 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
234 HGFCDKPEGECKRCRVGMQGRYCDCEIRYPCGLHGTCCQPMQCNCOBGWGLFCNODLNYCT 293
Qy 301 HHKPCKNAGATCTNTGQSYTCSRCRPGYTGNCCEIEVNECDANPCCKNGGSCDLENSYSC 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
294 HHKPCKNAGATCTNTGQSYTCSRCRPGYTGNCCEIEVNECDANPCCKNGGSCDLENSYSC 353
Qy 361 CPPGFGYKNCELSAMTADGPCFNGRGCTONPDGYSRCPLGYSGFNCCKKIDYCSSSP 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
354 CPPGFGYKNCELSAMTADGPCFNGRGCSDSPPDGYSCRCPCVGYSGFNCCKKIDYCSSSP 413
Qy 421 CANGAQCVDLGNYSYCOCQAGFTGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPG 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
414 CSNGAKCVDLDGAYLRCQAGFSRGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPG 473
Qy 481 NGKNCSTPVSRCBNPCHNGATCHERSNRYVCECARGYGGLNCOFLLPPEPQGPVVDFT 540
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
474 TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGLNCOFLLPPEPQGPVVDLT 533
Qy 541 EKYTEGQNSOPPIAVCAGIILVLMMLLGGCAAVVCLVLRKVKQRRHHPQACRSETETMN 600
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
534 EK-LEGQGGPPPVAVCAGIILVLMMLLGGCAAVVCLVLRKVKQRRHHPQACRSETETMN 592
Qy 601 LANCOREKDISISVIGATQIKNTNKKVDPHSDNS-DKNGYKVRYPVSDYNLVHELKNE 658
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
593 LANCOREKDISISVIGATQIKNTNKKVDPHSDNS-DKNGYKVRYPVSDYNLVHELKNE 652
Qy 659 SVKEHKGCEAKCETYSDEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
653 AVRNAHSKRTKCPQPGSSGSEKGTPTTLRGGSEASERKRPDSGCGSTSKDTKYQSVYVISE 712
Qy 718 KDECIITATEV 728
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
713 EKDECVIATEV 723
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RESULT 7
US-09-423-753-27
; Sequence 27, Application US/09423753
; Patent No. 6664098
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR
; FILE REFERENCE: KP-8693
; CURRENT APPLICATION NUMBER: US/09/423,753
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/JP98/02104
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 9/124064
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-753-27
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Query Match 84.1%; Score 3494.5; DB 4; Length 723;
Best Local Similarity 83.3%; Pred. No. 4.4e-255;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy 1 MGRFLTLTALLSALLCRCQVDSGVFELKQLQEFVNKGLLSNRNCCRGCGGPGGAGQOQC 60
Db 1 MGRSCALALAVLSALL--CQVSSGVFELKQLQEFVNKGLLSNRNCCR---GGAGPPPC 54
Qy 61 DCKTFFRVCLKHQYQASVSPPEPCTYGSATPVLGANSFSDVDPDAGGADPAFSPNIRPFG 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
55 ACRTFFRVCLKHQYQASVSPPEPCTYGSATPVLGANSFSDVDPDAGGADPAFSPNIRPFG 113
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QY 121 FTWPGTFSLIILALHTDSDPDLTTENPERLISRLATQRIHLAVGEWSQDLHSSGRTDLKY 180
DB 114 FTWPGTFSLIILALHTDSDPDLTTENPERLISRLATQRIHLAVGEWSQDLHSSGRTDLKY 173
QY 181 SYRFVDEHYHGGCVSFVCRPRDDRGHFTCGERKEKVCNPGWKGYCTEPICLPGCDEQ 240
DB 174 SYRFVDEHYHGGCVSFVCRPRDDRGHFTCGERKEKVCNPGWKGYCTEPICLPGCDEQ 233
QY 241 HGFCDKPGCKCRVWGQRYCDECIYPCGLHGTCCQWQCNQCBGWGLFCNQDLNYCT 300
DB 234 HGFCDKPGCKCRVWGQRYCDECIYPCGLHGTCCQWQCNQCBGWGLFCNQDLNYCT 293
QY 301 HHKPCNKGATCNTGOGSYTCSCRPYTGSSCEIEINCECDANPCNKGSCCTDLENSYCT 360
DB 294 HHKPCNKGATCNTGOGSYTCSCRPYTGATCELGIDECDPSPCKNGSGCTDLENSYCT 353
QY 361 CPPGFYGNKCELSAMTCADGPGCFNGGRCCTDNPDGYSRCPLGYSGFNCEKIDYCSSSP 420
DB 354 CPPGFYGNKCELSAMTCADGPGCFNGGRCSDSPDGYSRCPLGYSGFNCEKIDYCSSSP 413
QY 421 CANGAQCVDLGNSYICQCOAGTGRHCDNDVDDCASFPVNGGTCCQWQCNQCBGWGLFCNQDLNYCT 300
DB 414 CSNGAKCVDLGDAYLCRCQAGSFRHCDNDVDDCASFPVNGGTCCQWQCNQCBGWGLFCNQDLNYCT 293
QY 481 NGKNCSTPVSRCENHPCNCHGATCHEHSNRYCECARGYGLNCOFLPEPPGPGVVDFT 540
DB 474 TGRNCSAPVSRCEHAPCHNGATCHEHRYVCECARGYGLNCOFLPEPPGPGVVDFT 533
QY 541 EKYTEGQNSQFPWIAVCAGIILVLLMLLGCAGIIVVCRVLRKQHHQPCACRSETETMNN 600
DB 534 EK-LEQGGPFPWAVACAGIILVLLMLLGCAGIIVVCRVLRKQHHQPCACRSETETMNN 592
QY 601 LANCOREKDISISVIGATQIKNTNKKVDPHSDNS-DKNGYKVRYPVSDVNLVHKLKNEB- 658
DB 593 LANCOREKDISISVIGATQIKNTNKKADPHGDSADKNGFKARYPAVDVNLVQDLKGGDT 652
QY 659 SVKEHKGCEAKCETYDSEAEK-SAVOLKSDTSEKRPDSVYSTKDTKYQSVVYVISE 717
DB 653 AVRDAHSKRDTKCPQOGSSGEEKGPTTLRGGEASERKRPDSGCGSTSKDTKYQSVVYVISE 712

RESULT 8

US-10-140-002-346
; Sequence 346, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 346

; LENGTH: 723

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-002-346

Query Match 84.1%; Score 3494.5; DB 4; Length 723;

Best Local Similarity 83.3%; Pred. No. 4.4e-255;

Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCRQVDGSGVFELKLOEFVNNKGLLSNRNCCRGGGPGGAGQQOC 60

DB 1 MGRFLLTLALLSALLCRQVDGSGVFELKLOEFVNNKGLLSNRNCCRGGGPGGAGQQOC 54

QY 61 DCKTFRRVCLKHYQASVSPPEPTCYGSAITPVLGANSFVSPDGAGADPAFNPTRFPFG 120

DB 55 ACRTFFRVCLKHYQASVSPPEPTCYGSAITPVLGANSFVSPDGAGADPAFNPTRFPFG 113

QY 121 FTWPGTFSLIILALHTDSDPDLTTENPERLISRLATQRIHLAVGEWSQDLHSSGRTDLKY 180

DB 114 FTWPGTFSLIILALHTDSDPDLTTENPERLISRLATQRIHLAVGEWSQDLHSSGRTDLKY 173

QY 181 SYRFVDEHYHGGCVSFVCRPRDDRGHFTCGERKEKVCNPGWKGYCTEPICLPGCDEQ 240

DB 174 SYRFVDEHYHGGCVSFVCRPRDDRGHFTCGERKEKVCNPGWKGYCTEPICLPGCDEQ 233

QY 241 HGFCDKPGCKCRVWGQRYCDECIYPCGLHGTCCQWQCNQCBGWGLFCNQDLNYCT 300

DB 234 HGFCDKPGCKCRVWGQRYCDECIYPCGLHGTCCQWQCNQCBGWGLFCNQDLNYCT 293

QY 301 HHKPCNKGATCNTGOGSYTCSCRPYTGSSCEIEINCECDANPCNKGSCCTDLENSYCT 360

DB 294 HHKPCNKGATCNTGOGSYTCSCRPYTGATCELGIDECDPSPCKNGSGCTDLENSYCT 353

QY 361 CPPGFYGNKCELSAMTCADGPGCFNGGRCCTDNPDGYSRCPLGYSGFNCEKIDYCSSSP 420

DB 354 CPPGFYGNKCELSAMTCADGPGCFNGGRCSDSPDGYSRCPLGYSGFNCEKIDYCSSSP 413

QY 421 CANGAQCVDLGNSYICQCOAGTGRHCDNDVDDCASFPVNGGTCCQWQCNQCBGWGLFCNQDLNYCT 300

DB 414 CSNGAKCVDLGDAYLCRCQAGSFRHCDNDVDDCASFPVNGGTCCQWQCNQCBGWGLFCNQDLNYCT 293

QY 481 NGKNCSTPVSRCENHPCNCHGATCHEHSNRYCECARGYGLNCOFLPEPPGPGVVDFT 540

DB 474 TGRNCSAPVSRCEHAPCHNGATCHEHRYVCECARGYGLNCOFLPEPPGPGVVDFT 533

QY 541 EKYTEGQNSQFPWIAVCAGIILVLLMLLGCAGIIVVCRVLRKQHHQPCACRSETETMNN 600

DB 534 EK-LEQGGPFPWAVACAGIILVLLMLLGCAGIIVVCRVLRKQHHQPCACRSETETMNN 592

QY 601 LANCOREKDISISVIGATQIKNTNKKVDPHSDNS-DKNGYKVRYPVSDVNLVHKLKNEB- 658

DB 593 LANCOREKDISISVIGATQIKNTNKKADPHGDSADKNGFKARYPAVDVNLVQDLKGGDT 652

QY 659 SVKEHKGCEAKCETYDSEAEK-SAVOLKSDTSEKRPDSVYSTKDTKYQSVVYVISE 717

DB 653 AVRDAHSKRDTKCPQOGSSGEEKGPTTLRGGEASERKRPDSGCGSTSKDTKYQSVVYVISE 712

QY 718 EKDECIATEV 728

DB 713 EKDECIATEV 723

RESULT 9

US-08-872-855-7

; Sequence 7, Application US/08872855

; Patent No. 6121045

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean

; APPLICANT: Gearing, David

; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND

TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-855-7

Query Match 84.1%; Score 3491.5; DB 3; Length 721;
Best Local Similarity 82.1%; Pred. No. 7.4e-255;
Matches 599; Conservative 65; Mismatches 55; Indels 11; Gaps 7;
Qy 1 MGRFLTLTALLSALLCRQVDGSGVFELKLOEFVNNKGLLSNRNCRGGGPGG-AGQQQ 59
Db 1 MGQRMJTLVLAVL--CQISCSGLFELRLQEFVNNKGLLGNCCR---PGSLASLQR 55
Qy 60 CDCTFRVCLKHQVQASVSPPECTYGSATPVLGANSFSPVGDAGGADPAFSPNIRPPF 119
Db 56 CECKTFRICLKHQVNSVPEPTCYGAVTPVLGNSFVVPB--SSNADPTFSNIRPPF 114
Qy 120 GFTWPGTFLSLIEALHTDSPDLLTTPENPERLISRLATQRLHVLAVGEWSQDLHSSGRDCLK 179
Db 115 GFTWPGTFLSLIEALHTDSPDLLTTPENPERLISRLATQRLHVLAVGEWSQDLHSSDRTELK 174
Qy 180 YSYRFVCDHYHGGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDE 239
Db 175 YSYRFVCDHYHGGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGLYCTEPICLPGCDE 234
Qy 240 QHGFCDKPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGNGGLFCNQDLNYC 299
Db 235 HHGYCDKPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGNGGLFCNQDLNYC 294
Qy 300 THHKPCKNKATCTNTGQGSYTCSCRPGYTGSSCIEINECDANPCNKGSCDLENSYSC 359
Db 295 THHKPCKNKATCTNTGQGSYTCSCRPGYTGSSCIEINECDANPCNKGSCDLENSYTC 354
Qy 360 TCPPGFYGNKCELSAMTCAADGCPFNCGRCDTNPDDGYSRCPLGYSGFNCKKIDYCSSS 419
Db 355 SCPPGFYGNKCELSAMTCAADGCPFNCGRCDTNPDDGYSRCPLGYSGFNCKKIDYCSSN 414
Qy 420 PCANGAQCVDLGNYSYICOCQAGFTGRHCDNDVDDCASFPVNGGTCCDGVNDYSCTCPGG 479
Db 415 PCANGARCEDLGNYSYICOCQSGFSRNCDDNDLDCSTSPFCQNGGTCCDGVNDYSCTCPGG 474
Qy 480 YNGKNCSTPVSRCBHNPNCHNGATCHERSNRYVCECARGYGGLNCOFLLPPEQPPIVDF 539
Db 475 YIGKNCSTPVSRCBHNPNCHNGATCHERNRYVCECARGYGGLNCOFLLPPEQPPIVDF 532

Qy 540 TEKTEGQNSQFPMIAVCAGIILVLLMLLGCALVVCVRLKVQKRHHQPEACRSETETMN 599
Db 533 TEKTEGQSGQFPMIAVCAGIILVLLMLLGCALVVCVRLKVQKRHHQPEACRSGSKTMN 592
Qy 600 NLANCQREKDISISVIATQIKNTNKKVDPHSD--NSDKNGYKVRYPSPVDYVNLVHKLKNEB 658
Db 593 NLANCQREKDISISVFIGTQTQKNTNKKIDFLSESNNEKNKYKPRYPSPVDYVNLVHKLKNEB 652
Qy 659 SVKEEHKGRKAKCTYDSEAEKSAVOLKSSDTSERKRPDSVYSTKDTKYQSVVVISSE 718
Db 653 SPKEERSKCEAKSSNDSDESVNSVHSK--RDSERRRRPDSAYSTKDTKYQSVTVISDE 711
Qy 719 KDECIITATEV 728
Db 712 KDECIITATEV 721
RESULT 10
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641.612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-6

Query Match 83.5%; Score 3466.5; DB 4; Length 723;
Best Local Similarity 82.8%; Pred. No. 5.7e-253;
Matches 605; Conservative 47; Mismatches 68; Indels 11; Gaps 7;
Qy 1 MGRFLTLTALLSALLCRQVDGSGVFELKLOEFVNNKGLLSNRNCRGGGPGGAGQQQC 60
Db 1 MGRSCALALAVLSALL--CQVWSSGVFELKLOEFVNNKGLLGNPCCR---GGAGPPPC 54
Qy 61 DCKTFRVCLKHQVQASVSPPECTYGSATPVLGANSFSPVGDAGGADPAFSPNIRPPFG 120
Db 55 ACRTFRVCLKHQVQASVSPPECTYGSATPVLGVDVSFLPDG--GGADSAFSPNIRPPFG 113
Qy 121 FTWPGTFLSLIEALHTDSPDLLTTPENPERLISRLATQRLHVLAVGEWSQDLHSSGRDCLKY 180
Db 114 FTWPGTFLSLIEALHTDSPDLLTTPENPERLISRLATQRLHVLAVGEWSQDLHSSGRDCLKY 173
Qy 181 YSYRFVCDHYHGGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDEQ 240
Db 174 YSYRFVCDHYHGGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDBQ 233
Qy 241 HGFCDKPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGNGGLFCNQDLNYCT 300
Db 234 HGFCDKPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGNGGLFCNQDLNYCT 293
Qy 301 HHKPCKNKATCTNTGQGSYTCSCRPGYTGSSCIEINECDANPCNKGSCDLENSYSC 360
Db 294 HHKPCKNKATCTNTGQGSYTCSCRPGYTGATCELGIDECDDPSCKNGSGCDLENSYSC 353
Qy 361 CPPGFYGNKCELSAMTCAADGCPFNCGRCDTNPDDGYSRCPLGYSGFNCKKIDYCSSSP 420
Db 354 CPPGFYGNKCELSAMTCAADGCPFNCGRCDSDSPDGYSRCPLGYSGFNCKKIDYCSSSP 413
Qy 421 CANGAQCVDLGNYSYICOCQAGFTGRHCDNDVDDCASFPVNGGTCCDGVNDYSCTCPGGY 480
Db 414 CSNGAKCVDLGDYALCKQAGFSGRHCDNDVDDCASFPANGGTCTCRGVNDVDFCTCTCPGGY 473
Qy 481 NGKNCSTPVSRCBHNPNCHNGATCHERSNRYVCECARGYGGLNCOFLLPPEQPPIVDF 540

Db 474 TGRNCAPVSRCEHACHNGATCHERGHVCECARGYGPNCQFLLPELPGPAVVDLT 533
QY 541 EKYTEQNSQFPWIAVCAGIILVLLGCAAIIVCVRLKVKQRHHQPEACRSETETMNN 600
Db 534 EK-LEGQGGPFPWAVACAGIILVLLGCAAVVVCPLRLQKRPADPCRGETETMNN 592
QY 601 LANCOREKDISVIGATQIKNTNKKVDPHSDNS-DKNGYKVRYPVDVNLVHELKNE- 658
Db 593 LANCOREKDISVIGATQIKNTNKKADFHGDSADKNGFKARYPAVDVNLVQDLKGDPT 652
QY 659 SYKEEHGKCEAKCETVDSAEK-SAVOLKSSDTSERKRPDSVYSTKDTKYQSVVIVISE 717
Db 653 AVRDASHKRTKCPQOGSSGEEKGTPTTLRGGEASERKRPDSCGTSKDTKYQSVVIVISE 712
QY 718 EXDECIATEV 728
Db 713 EXDECVIATEV 723

RESULT 11
US-09-068-740A-4
; Sequence 4, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-068-740A-4

Query Match 83.0%; Score 3445.5; DB 3; Length 702;
Best Local Similarity 84.0%; Pred. No. 2.1e-251;
Matches 595; Conservative 46; Mismatches 58; Indels 9; Gaps 6;
QY 24 SGVFELKLOEFVNNKGLLNRCRGGGPGGAGQOQCDCTFRVCLKHQYQASVPEPPC 83
Db 1 SGVFELKLOEFVNNKGLLNRCR---GGAGPPPCACRTFRVCLKHQYQASVPEPPC 56
QY 84 TYGSAITPVLGANSFVPGGAGADPAFNPTRFPFGFTWPGTFSIIIEALHTDSDPDLT 143
Db 57 TYGSAITPVLGVSFSLPG-GGADSAFNPTRFPFGFTWPGTFSIIIEALHTDSDPDLA 115
QY 144 TENPERLISRLATQRLHVLAGEWSQDLHSGRTDLKYSYRFVCDHYHGGCVFCRPRD 203
Db 116 TENPERLISRLATQRLHVLAGEWSQDLHSGRTDLKYSYRFVCDHYHGGCVFCRPRD 175
QY 204 DRFGHFTCGERKVCNPGWKGQYCTEPICLPGCDEHQGFCDKPGCKCRVGMQRYCDE 263
Db 176 DAFGHFTCGERKVCNPGWKGQYCTEPICLPGCDEHQGFCDKPGCKCRVGMQRYCDE 235
QY 264 CIRYPGCLHGTCCOOPWQNCQEGWGLFCNQDLNYCTHHKPCKNGATCTNTGGSYTCS 323
Db 236 CIRYPGCLHGTCCOOPWQNCQEGWGLFCNQDLNYCTHHKPCKNGATCTNTGGSYTCS 295
QY 324 RPYGTSSCEIENECDANPCNKGSGCTDLNSYCTCPPGFYGNKNCELSAMTCADGPCF 383
Db 296 RPYGTGATCGLGIDECPSPCKNGSGCTDLNSYCTCPPGFYGNKNCELSAMTCADGPCF 355

QY 384 NGRCTDNPDDGYSRCRPLGYSGFNCEKKIDYCSSSPCANGAQCVDLGNSTYCCOAGFT 443
Db 356 NGRCSDSPDGYSRCRPLGYSGFNCEKKIDYCSSSPCANGAKCVDLGDAYLCRCOAGFS 415
QY 444 GRHCDNDVDDCASPFCVNGGTCQDQGVNDYSTCTPPGYNGKNCSTPVSRCEHNPCHNGATC 503
Db 416 GRHCDNDVDDCASPFCANGGTCTCRDGVNDYSTCTPPGYTGRNCSPAIVSRCEHAPCHNGATC 475
QY 504 HERSNRYVCECARGVGLNCQFLLPEPQGPVIVDFTEKYTEGQNSQFPWIAVCAGIILV 563
Db 476 HERGHRYVCECARGVGGPNCQFLLPELPGPAVVDLT-LEGQGGPFPWAVACAGIILV 534
QY 564 LMLLGCACAIIVCVRLKVKQRHHQPEACRSETETMNNLANCOREKDISVIGATQIKNT 623
Db 535 LMLLGCACAAVVCVRLRLQKRPADPCRGETETMNNLANCOREKDISVIGATQIKNT 594
QY 624 NKKVDPHSDNS-DKNGYKVRYPVDVNLVHELKNE-SYKEEHGKCEAKCETVDSAEK 681
Db 595 NKKADFHGDSADKNGFKARYPAVDVNLVQDLKGDPTAVRDAHSKRDTCQCPQGSSEK 654
QY 682 -SAVOLKSSDTSERKRPDSVYSTKDTKYQSVVIVISEEKDECIATEV 728
Db 655 GTPTTLRGGEASERKRPDSCGTSKDTKYQSVVIVISEEKDECVIATEV 702

RESULT 12
US-08-872-855-4
; Sequence 4, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-4

Query Match 81.3%; Score 3375; DB 3; Length 720;
Best Local Similarity 79.2%; Pred. No. 4.4e-246;
Matches 579; Conservative 71; Mismatches 67; Indels 14; Gaps 8;
QY 1 MGRFLLTALLSALLCRCQVDGSGVFELKLOEFVNNKGLLNRCRGG-GPGGAGQOO 59

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Db      1 MGRSALALAVVSALL--CQWSSGVFELKQLQEFVNKKGLGNRNCCRGSGP-----P 52
Qy      60 CDCKTFRRVCLKHVQASVSEPPCTYGSATTPVLGANSFSVPDAGGADPAFSPNIRPPF 119
Db      53 CACRTFFRVCLKH-QASVSEPPCTYGSATTPVLGVSFSLPDGA-GIDPAFSPNIRPPF 110
Qy      120 GFTWPGTFLSLIEALHTSDPDLTTPENPERLISRLATQRLHVAEGEWSQDLHSSGRTDLK 179
Db      111 GFTWPGTFLSLIEALHTSDPDLATENPERLISRLTQRLH-TVGEWSQDLHSSGRTDLR 169
Qy      180 YSYRFVCDHYHYGEGSVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDE 239
Db      170 YSYRFVCDHYHYGEGSVFCRPRDFAFHFTCGDRGEKVCNPGWKGOYCTDPICLPGCDD 229
Qy      240 QHGFCDKPGCKRVMGGRYCDCEIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYC 299
Db      230 QHGFCDKPGCKRVMGGRYCDCEIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYC 289
Qy      300 THHKPCRNKGTCTNTGQSYTCSCRPGYTGSSCIEINECDANPCNKGSGCTDLENSYSC 359
Db      290 THHKPCRNKGTCTNTGQSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSC 349
Qy      360 TCPGFGYKNCNELSAMTCADGCPFCNGGRCCTDNDPGGYSCRCPLGYSGFNCEKKIDYCSS 419
Db      350 TCPGFGYKNCNELSAMTCADGCPFCNGGRCSDNPDGGYTCCHPLGFSGFNCEKKMDLCCSS 409
Qy      420 PCANGAOCVDLGNYSYICOCQAGFTGRHCDNDVDCAFPCCVNGGTCCODGVNDYSCTCPG 479
Db      410 PCSNGAKCVDLGNYSYLCRCQAGFSRYCEDNVDCAFPCCANGGTCTDSDVNDFSCTCPG 469
Qy      480 YNGKNCSTPVSRCENHPCHNGATCHERSNRNYVCRCARGYGLNCQFLLPEPPGQPIVDF 539
Db      470 YTGKNCAPVSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCQFLLPEPPGPMVVDL 529
Qy      540 TEKYTEGQNSQPPWIAVCAGIILVLLGCAAVVVCVRLKVKQRHHQPEACRSETETMN 599
Db      530 SERHMSQGGPFPWAVACAGVLLVLLGCAAVVVCVRLKQKHQPPPEPCGGETETMN 589
Qy      600 NLANCOREKDISIVIGATOIKNTNKKVDFHSDN-SDKNGYKVRYPVDYNLHVK-NE 657
Db      590 NLANCOREKDVSVIIGATOIKNTNKKADFHGDHGAKKSFVKRYPTVDYNLVRDLKGDE 649
Qy      658 DSVKEBHGKCEAKCETYSDBAEBSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717
Db      650 ATVRDTHSKRDKCSQSSAGEEKIAPTLARGEIPDRKRPSVYSTSKDTKYQSVYVLSA 709
Qy      718 EKDECIATEV 728
Db      710 EKDECIATEV 720

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RESULT 13

```

US-08-981-392-12
; Sequence 12, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Isakona, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

```

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-392-12

Query Match      81.1%; Score 3368; DB 3; Length 722;
Best Local Similarity 78.5%; Pred. No. 1.5e-245;
Matches 574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;

Qy      1 MGRFLTLTALLSALLCRCQVDGSGVFELKQLQEFVNKKGLGNRNCCRGG-GPGAGAGQQ 59
Db      1 MGRSALALAVVSALL--CQWSSGVFELKQLQEFVNKKGLGNRNCCRGSGP-----P 52
Qy      60 CDCKTFRRVCLKHVQASVSEPPCTYGSATTPVLGANSFSVPDAGGADPAFSPNIRPPF 119
Db      53 CACRTFFRVCLKHVQASVSEPPCTYGSATTPVLGVSFSLPDGA-GIDPAFSPNIRPPF 111
Qy      120 GFTWPGTFLSLIEALHTSDPDLTTPENPERLISRLATQRLHVAEGEWSQDLHSSGRTDLK 179
Db      111 GFTWPGTFLSLIEALHTSDPDLATENPERLISRLTQRLH-TVGEWSQDLHSSGRTDLR 171
Qy      180 YSYRFVCDHYHYGEGSVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDE 239
Db      172 YSYRFVCDHYHYGEGSVFCRPRDFAFHFTCGDRGEKVCNPGWKGOYCTDPICLPGCDD 231
Qy      240 QHGFCDKPGCKRVMGGRYCDCEIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYC 299
Db      232 QHGFCDKPGCKRVMGGRYCDCEIRYPGCVNGTCCQPMQCNCQEGWGLFCNQDLNYC 291
Qy      300 THHKPCRNKGTCTNTGQSYTCSCRPGYTGSSCIEINECDANPCNKGSGCTDLENSYSC 359
Db      292 THHKPCRNKGTCTNTGQSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSC 351
Qy      360 TCPGFGYKNCNELSAMTCADGCPFCNGGRCCTDNDPGGYSCRCPLGYSGFNCEKKIDYCSS 419
Db      352 TCPGFGYKNCNELSAMTCADGCPFCNGGRCSDNPDGGYTCCHPLGFSGFNCEKKMDLCCSS 411
Qy      420 PCANGAOCVDLGNYSYICOCQAGFTGRHCDNDVDCAFPCCVNGGTCCODGVNDYSCTCPG 479
Db      412 PCSNGAKCVDLGNYSYLCRCQAGFSRYCEDNVDCAFPCCANGGTCTDSDVNDFSCTCPG 471
Qy      480 YNGKNCSTPVSRCENHPCHNGATCHERSNRNYVCRCARGYGLNCQFLLPEPPGQPIVDF 539
Db      472 YTGKNCAPVSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCQFLLPEPPGPMVVDL 531
Qy      540 TEKYTEGQNSQPPWIAVCAGIILVLLGCAAVVVCVRLKVKQRHHQPEACRSETETMN 599
Db      532 SERHMSQGGPFPWAVACAGVLLVLLGCAAVVVCVRLKQKHQPPPEPCGGETETMN 591
Qy      600 NLANCOREKDISIVIGATOIKNTNKKVDFHSDN-SDKNGYKVRYPVDYNLHVK-NE 657
Db      592 NLANCOREKDVSVIIGATOIKNTNKKADFHGDHGAKKSFVKRYPTVDYNLVRDLKGDE 651
Qy      658 DSVKEBHGKCEAKCETYSDBAEBSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717

```


TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-855-5

Query Match 80.6%; Score 3346.5; DB 3; Length 713;
Best Local Similarity 78.5%; Fred. No. 6.2e-244;
Matches 574; Conservative 67; Mismatches 69; Indels 21; Gaps 8;

QY 1 MGRFLLTLALLSALLCQVDGQVDFVFNKGLLSNRNCRGG-GPGGAGQQQ 59
DB 1 MGRSALALAVSALL--CQWSSGVFELKQEFVFNKGLLGNRNCCRGSGP-----P 52

QY 60 CDCKTFFRVCLKHQASVSPEPPCTYGSATPVLGANSFSPDGAGGADPAFSPNPIRPPF 119
DB 53 CACRTFFRVCLKHQASVSPEPPCTYGSATVAVLGVDSFSLPDGA-GIDPAFSPNPIRPPF 111

QY 120 GFTWPGTSLIEALHTSPDGLTTENPERLISRLATORHLAVGEWSQDLHSSGRTDLK 179
DB 112 GFTWPGTSLIEALHTSPDGLTTENPERLISRLATQTH-TVGEWSQDLHSSGRTDLR 170

QY 180 YSYRFVCDHYHGECSVFCRPRDRFGHFTCGERGEKVCNPGWKQYCTEPICLPGCCDE 239
DB 171 YSYRFVCDHYHGECSVFCRPRDDAFGHFTCGERGEKVCNPGWKQYCTEPICLPGCCDD 230

QY 240 QHGFCDKPECKRCRVGMGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWGGLFCNQDLNYC 299
DB 231 QHGFCDKPECKRCRVGMGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWGGLFCNQDLNYC 290

QY 300 THHKPCNKATCTYTGQSYTCSRCRPGYTGSCEIEINECDANPCNKGSCDLDLSYSC 359
DB 291 THHKPCNKATCTYTGQSYTCSRCRPGYTGANCELEVDCAFPCKNGSCDLDLSYSC 350

QY 360 TCPGFGYKNCBLSAMTCAAGPCFNGRCCTNPDGYSRCPLGYSGFNCCKKIDYCSSS 419
DB 351 TCPGFGYKNCBLSAMTCAAGPCFNGRCSDNPDGGYTCHCPAGFSGFCNCKKIDLCSSS 410

QY 420 PCANGAQCVDLGNYSYICOCAGFTGRHCDNDVDCASPPCVNNGGTCODGVNDYSCTCPPG 479
DB 411 PCSNGAKCVDLGNYSYLCRCQTGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 470

QY 480 YNGKNCSTPVSRCBHPCHNGATCHERSNRYVCECARGYGLNCOFLLPEPPQGPVIVDF 539
DB 471 YTGKNCAPVSRCBHPCHNGATCHQRQRYMCECAQGYGGANCOFLLPEPPDLIVA-- 528

QY 540 TEKYTEGONSOPPMIYAVCAGIILVLLGLCAAIVCVRLKVKRHHQPEACRSETMTN 599
DB 529 -----AQGGSPWVAVCAGVVLVLLGLCAAIVCVRLKQHQPPDPCCGGTETMN 582

QY 600 NLANCQREKDISIVIGATQIKNTNKKVDVDFHSDN-SDKNGYKVRYPYVDVNLVHKLK-NE 657
DB 583 NLANCQREKDVSVIIGATQIKNTNKKADPHGDHGAADKSPKARYPTVDVNLIRDLKGE 642

QY 658 DSVKBEHGKCAKETVDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717
DB 643 ATVRDAHSKRDTKQSQSAGEEKSSTLRGGEVDRKRPRSVYSTSKDTKYQSVYVLSA 702

QY 718 EKDECIATEV 728
DB 703 EKDECVIATEV 713

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:11:34 ; Search time 76.5563 Seconds
(without alignments)
3411.281 Million cell updates/sec

Title: US-09-783-931-2

Perfect score: 4153

Sequence: 1 MGGRFLTLALLSALLCRQC.....YQSVYVISEKDECIATEV 728

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4153	100.0	740	2	AAW00876
2	4119.5	99.2	727	2	AAW11719
3	4108	98.9	728	3	AAV79029
4	3494.5	84.1	723	2	AAW18353
5	3494.5	84.1	723	2	AAW75492
6	3494.5	84.1	723	2	AAW94498
7	3494.5	84.1	723	3	AAV83227
8	3494.5	84.1	723	3	AAV83227
9	3494.5	84.1	723	3	AAV83227
10	3494.5	84.1	723	3	AAV83227
11	3494.5	84.1	723	4	AAU12344
12	3494.5	84.1	723	4	AAU12344
13	3494.5	84.1	723	4	AAU12344
14	3494.5	84.1	723	6	ABO17788
15	3494.5	84.1	723	6	ABU66742
16	3494.5	84.1	723	6	ABU66742
17	3494.5	84.1	723	6	ABU59823
18	3494.5	84.1	723	6	ABO25013
19	3494.5	84.1	723	6	ABU67018
20	3494.5	84.1	723	6	ADA45865
21	3494.5	84.1	723	6	ADA76296
22	3494.5	84.1	723	6	ADA18946
23	3494.5	84.1	723	6	ADA61569
24	3494.5	84.1	723	6	ADB13354
25	3494.5	84.1	723	6	ADA86374

26	3494.5	84.1	723	6	ADB15938	Human PRO
27	3494.5	84.1	723	6	ADA47724	Human PRO
28	3494.5	84.1	723	6	ADA67519	Human PRO
29	3494.5	84.1	723	6	ADB30526	Human PRO
30	3494.5	84.1	723	6	ADA85822	Novel hum
31	3494.5	84.1	723	6	ADA97034	Human PRO
32	3494.5	84.1	723	6	ADA79338	Human PRO
33	3494.5	84.1	723	6	ADA87477	Novel hum
34	3494.5	84.1	723	6	ADB16679	Human PRO
35	3494.5	84.1	723	6	ADA91771	Novel hum
36	3494.5	84.1	723	6	ADB14834	Human PRO
37	3494.5	84.1	723	6	ADB18795	Novel hum
38	3494.5	84.1	723	6	ADA94010	Human PRO
39	3494.5	84.1	723	6	ADB19906	Novel hum
40	3494.5	84.1	723	6	ADB13218	Human PRO
41	3494.5	84.1	723	6	ABO43321	Novel hum
42	3494.5	84.1	723	6	ADA74472	Human PRO
43	3494.5	84.1	723	6	ADB24705	Human PRO
44	3494.5	84.1	723	6	ADA82229	Human PRO
45	3494.5	84.1	723	6	ADA75192	Human PRO

ALIGNMENTS

RESULT 1
AAW00876
ID AAW00876 standard; protein; 740 AA.

XX AC AAW00876;

DT 28-APR-1997 (first entry)

DE C-Delta-1 polypeptide (alternatively spliced variant).

XX C-Delta-1; cell proliferation; nervous system disorder;
KW tissue regeneration; Notch; cervix cancer; breast cancer;
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.

OS Gallus sp.

XX Key Location/Qualifiers

FT Domain 184..228

FT Domain /label= DSL

FT Domain 229..261

FT Domain /label= EGF1

FT Domain 262..292

FT Domain /label= EGF2

FT Domain 293..332

FT Domain /label= EGF3

FT Domain 333..370

FT Domain /label= EGF4

FT Domain 371..409

FT Domain /label= EGF5

FT Domain 410..447

FT Domain /label= EGF6

FT Domain 448..485

FT Domain /label= EGF7

FT Domain 486..523

FT Domain /label= EGF8

FT Domain 524..534

FT Domain /label= EGF9

FT Domain 555..579

FT Domain /label= TM

FT /note= "transmembrane domain"

XX WO9701571-A1.

XX 16-JAN-1997.

XX 28-JUN-1996; 96WO-US011178.

XX 28-JUN-1995; 95US-0000589P.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA (UYIA) UNIV YALE.
XX
PI Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;
XX Gray GE;
XX WPI; 1997-100159/09.
DR N-PSDB; AAT58898.
XX
PT New vertebrate Delta protein, DNA and antibodies - for treating and
PT preventing cancer, nervous system disorders and for tissue regeneration.
XX
PS Disclosure; Fig 2; 135pp; English.
XX
CC C-delta-1 polypeptide (AAW00876) is the chick homologue of Drosophila
CC Delta, a protein that binds to Notch protein. Expression of C-Delta-1
CC correlates with onset of neurogenesis. The C-delta-1 amino acid sequence
CC was deduced from a cDNA clone (AAT58898) obtd. from chick stage 4-6
CC embryos. A shorter version (AAW58877) of C-Delta-1, lacking the 12 C-
CC terminal amino acids of the longer version, was also isolated, and mouse
CC (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have been
CC identified. Delta-1 proteins can be used to treat or prevent disorders
CC characterised by increased Notch activity, such as cervical, breast, lung
CC or colon cancer, melanoma or seminoma, and nervous system disorders or to
CC promote tissue regeneration and repair
XX
SQ Sequence 740 AA;

Query Match 100.0%; Score 4153; DB 2; Length 740;
Best Local Similarity 100.0%; Pred. No. 7.2e-228;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQLQFVNKGLLSNRNCCRGCGPGAGQQQC 60
DB 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQLQFVNKGLLSNRNCCRGCGPGAGQQQC 60

QY 61 DCKTFRVCLKHQVQSVSPPTCTYSATTPVLGANSFSPDGAGADPAFNPFRPFG 120
DB 61 DCKTFRVCLKHQVQSVSPPTCTYSATTPVLGANSFSPDGAGADPAFNPFRPFG 120

QY 121 FTWPGTFSLLIEALHTDSPDLLTTPENPERLSLQRLAVGEWSQLHSSGRDLYK 180
DB 121 FTWPGTFSLLIEALHTDSPDLLTTPENPERLSLQRLAVGEWSQLHSSGRDLYK 180

QY 181 SYRFVDEHYHGGCSVFCRPRDRFGHTFCGERGEKVCNPGWKQYCTEPICLPGCDSQ 240
DB 181 SYRFVDEHYHGGCSVFCRPRDRFGHTFCGERGEKVCNPGWKQYCTEPICLPGCDSQ 240

QY 241 HGFCDKPGCKRCHVQGRYCDICIRYPCGLHGTCCQPHQCNCOEGWGLFCNODLNYCT 300
DB 241 HGFCDKPGCKRCHVQGRYCDICIRYPCGLHGTCCQPHQCNCOEGWGLFCNODLNYCT 300

QY 301 HHKPCXNGATCTNTGGSVYTCRCRPGYTGSSCEIENECDANPKNGSGCTDLENSYCT 360
DB 301 HHKPCXNGATCTNTGGSVYTCRCRPGYTGSSCEIENECDANPKNGSGCTDLENSYCT 360

QY 361 CPPGFYGNKCELSAMTCADGPCFNGRCCTDNDGGYSCRCPLGYSGFNCEKIDYCSSP 420
DB 361 CPPGFYGNKCELSAMTCADGPCFNGRCCTDNDGGYSCRCPLGYSGFNCEKIDYCSSP 420

QY 421 CANGACVDLGNYSYICQAGFTGRHCDNDVDCASFPVNGGTCCDGVNDYSCTCPGY 480
DB 421 CANGACVDLGNYSYICQAGFTGRHCDNDVDCASFPVNGGTCCDGVNDYSCTCPGY 480

QY 481 NGKNCSTPVSRCBNHCHNGATCHERSNRYVCRCARGYGLNCQFLLPBPQGPVVDFT 540
DB 481 NGKNCSTPVSRCBNHCHNGATCHERSNRYVCRCARGYGLNCQFLLPBPQGPVVDFT 540

QY 541 EKYTEGNSQFPWIAVCAGIILVLLGLGCAAILVVCRLKVKQRHHPQACRSETTMN 600
DB 541 EKYTEGNSQFPWIAVCAGIILVLLGLGCAAILVVCRLKVKQRHHPQACRSETTMN 600

QY 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVDYNLVHELKNEEDSV 660
DB 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVDYNLVHELKNEEDSV 660

QY 661 KEEHGKCEAKCTYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVIVSEKX 720
DB 661 KEEHGKCEAKCTYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVIVSEKX 720

QY 721 ECIIATEV 728
DB 721 ECIIATEV 728

RESULT 2
AAW11719
ID AAW11719 standard; protein; 727 AA.
XX
AC AAW11719;
XX
DT 28-APR-1997 (first entry)
XX
DE C-Delta-1 polypeptide.
XX
KW C-Delta-1; cell proliferation; nervous system disorder;
KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.
XX
OS Gallus sp.

FH Key Location/Qualifiers
FT Domain 184..228 /label= DSL
FT Domain 229..261 /label= EGF1
FT Domain 262..292 /label= EGF2
FT Domain 293..332 /label= EGF3
FT Domain 333..370 /label= EGF4
FT Domain 371..409 /label= EGF5
FT Domain 410..447 /label= EGF6
FT Domain 448..485 /label= EGF7
FT Domain 486..523 /label= EGF8
FT Domain 524..534 /label= EGF9
FT Domain 555..579 /label= TM
FT /note= "transmembrane domain"

XX WO9701571-A1.
XX
XX 16-JAN-1997.
XX
XX 28-JUN-1996; 96WO-US011178.
XX
XX 28-JUN-1995; 95US-0000589P.
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA (UYIA) UNIV YALE.
XX
XX Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;
XX Gray GE;
XX WPI; 1997-100159/09.
DR N-PSDB; AAT58897.
XX
PT New vertebrate Delta protein, DNA and antibodies - for treating and
PT preventing cancer, nervous system disorders and for tissue regeneration.

XX	PS	Disclosure; Fig 2; 135pp; English.
XX	CC	C-delta-1 polypeptide (AAW11719) is the chick homologue of Drosophila
XX	CC	Delta, a protein that binds to Notch protein. Expression of C-delta-1
XX	CC	correlates with onset of neurogenesis. The C-delta-1 amino acid sequence
XX	CC	was deduced from a cDNA clone (AAT58897) obtd. from chick stage 4-6
XX	CC	embryos. An alternatively spliced variant (AAW00876) was also isolated,
XX	CC	and mouse (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have
XX	CC	been identified. Delta-1 proteins can be used to treat or prevent
XX	CC	disorders characterised by increased Notch activity, such as cervical,
XX	CC	breast, lung or colon cancer, melanoma or seminoma, and nervous system
XX	CC	disorders or to promote tissue regeneration and repair
XX	SQ	Sequence 727 AA;
		Query Match 99.2%; Score 4119.5; DB 2; Length 727;
		Best Local Similarity 99.6%; Pred. No. 5.7e-226;
		Matches 725; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy	1	MGRFLTLTALLSALLCRQVDGSGVFELKQEFVFNKGLLSNRNCCRGSGGAGGQOQC 60
Db	1	MGRFLTLTALLSALLCRQVDGSGVFELKQEFVFNKGLLSNRNCCRGSGGAGGQOQC 60
Qy	61	DKTFFRVLKXYQASVSPPECTYGSAITPVLGANSFVDPGAGGADPAFNSPIRPFPG 120
Db	61	DKTFFRVLKXYQASVSPPECTYGSAITPVLGANSFVDPGAGGADPAFNSPIRPFPG 120
Qy	121	FTWGTSLIIEALHTDSPDILTENPERLLSRLATQRLHLAGVSEWSQDLHSSGRTDKY 180
Db	121	FTWGTSLIIEALHTDSPDILTENPERLLSRLATQRLHLAGVSEWSQDLHSSGRTDKY 180
Qy	181	SYRVCDDEHYGEGSVFCRRDRDFGHFTGCEGKVCNPGWKGOYCTEPICLPGDDEQ 240
Db	181	SYRVCDDEHYGEGSVFCRRDRDFGHFTGCEGKVCNPGWKGOYCTEPICLPGDDEQ 240
Qy	241	HGFCDKPGECKRVGMQGRYDCBIRYPGCLHGTCCQPMQCNQCGMGGLFCNDLNYCT 300
Db	241	HGFCDKPGECKRVGMQGRYDCBIRYPGCLHGTCCQPMQCNQCGMGGLFCNDLNYCT 300
Qy	301	HHKCKNGATCTNTGQSYTSCRPYTGSSCEIIEINECNDANPCNKGSCSTDLENSYCT 360
Db	301	HHKCKNGATCTNTGQSYTSCRPYTGSSCEIIEINECNDANPCNKGSCSTDLENSYCT 360
Qy	361	CPPGFYGNKCELSAMTADGFCFNGRCRTDNPDGYSRCPLGYSGFNCKEKKIDYCS SSP 420
Db	361	CPPGFYGNKCELSAMTADGFCFNGRCRTDNPDGYSRCPLGYSGFNCKEKKIDYCS SSP 420
Qy	421	CANGAQCVDLGNYSYCQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY 480
Db	421	CANGAQCVDLGNYSYCQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY 480
Qy	481	NGKNCSTPVSCEINPCHNGATCHERSNRYVCECARGYGGLNCFLLPPEPQGVIVDFT 540
Db	481	NGKNCSTPVSCEINPCHNGATCHERSNRYVCECARGYGGLNCFLLPPEPQGVIVDFT 540
Qy	541	EKYTEGQNSQFPMTAVCAGIILVLLGLGCAIIVCVRLKVQKRHOPACRSSTETMNN 600
Db	541	EKYTEGQNSQFPMTAVCAGIILVLLGLGCAIIVCVRLKVQKRHOPACRSSTETMNN 599
Qy	601	LANCOREKDISISVIGATQIKNTNKKVDPHSDNSDKNGYKVRYPVSNLVHLELNEDSV 660
Db	600	LANCOREKDISISVIGATQIKNTNKKVDPHSDNSDKNGYKVRYPVSNLVHLELNEDSV 659
Qy	661	KEHGKCEAKCETVDSAEBSAVQLKSSDTSERKRDPDSVYSTKDTKYQSVYVISEKD 720
Db	660	KEHGKCEAKCETVDSAEBSAVQLKSSDTSERKRDPDSVYSTKDTKYQSVYVISEKD 719
Qy	721	ECIIATEV 728
Db	720	ECIIATEV 727

RESULT 3	
AAV79029	AAV79029 standard; protein; 728 AA.
XX	AAV79029;
XX	AAV79029;
DT	06-JUN-2000 (first entry)
XX	Chick delta protein amino acid sequence.
DE	
XX	Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;
KW	lung; melanoma; seminoma; central nervous system disorder; psoriasis;
KW	tissue regeneration; liver cirrhosis; keloid formation; baldness;
KW	inner ear disorder; chick.
XX	
OS	Gallus sp.
XX	
FN	WO200002897-A2.
XX	
PD	20-JAN-2000.
XX	
XX	13-JUL-1999; 99WO-USO15817.
XX	
PR	13-JUL-1998; 98US-0092513P.
PR	19-OCT-1998; 98US-0104834P.
XX	
XX	(UYVA) UNIV YALE.
XX	
PI	Artavanis-Tsakonas S, Rand MD, Qi H;
XX	
XX	WPI; 2000-282852/24.
XX	
PT	New cleavage peptide, nucleic acids and antibodies useful for diagnosis,
PT	prevention and treatment of cancer, disorders of central nervous system,
PT	cirrhosis and psoriasis.
XX	
PS	Claim 1; Fig 3; 177pp; English.
XX	
XX	This sequence represents the chick delta protein amino acid sequence.
CC	Delta is a topothymic protein that contains a sequence which is cleaved
CC	by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz
CC	results in two fragments, a soluble amino terminal fragment consisting
CC	essentially of the extracellular domain, and a membrane bound fragment
CC	consisting of the transmembrane domain and the intracellular domain. The
CC	soluble fragment is able to bind to Notch. Delta plays a key role in
CC	differentiation, and therefore detection and measurement of delta
CC	activation is important in the study of differentiation. The invention
CC	relates to the delta cleavage peptides (the active fragment), and to
CC	methods for detecting and measuring delta activation. Delta cleavage
CC	peptides, and chimeric proteins are useful for modulating the activity of
CC	Notch, delta or kuz or at least one of the signalling pathways in a cell
CC	or organism, expressing Notch. By contacting a cell with kuz protein or
CC	nucleic acid or its antibody, the activity or levels of delta protein is
CC	modulated and vice versa. A delta cleavage peptide or its derivative
CC	capable of binding kuz protein is useful for treating or preventing a
CC	disease or disorder associated with increased delta activity or
CC	expression such as cervical, breast, colon or lung cancer, melanoma or
CC	seminoma in humans. A recombinant cell comprising a delta peptide is
CC	useful for treating or preventing central nervous system disorders. A
CC	delta cleavage peptide is useful for the diagnosis of diseases or
CC	disorders associated with increased levels of Notch-delta protein binding
CC	activity comprising measuring the ability of delta cleavage peptides in a
CC	sample to bind kuz protein. A complex of delta protein and kuz is useful
CC	for diagnosing or screening for the presence of, or predisposition to
CC	developing a disease or disorder associated with aberrant levels of the
CC	complex, comprising measuring the level or functional activity of the
CC	complex or RNA encoding delta or kuz in a sample. The delta cleavage
CC	peptide is also useful for promoting tissue regeneration and repair, for
CC	treating liver cirrhosis, keloid formation, psoriasis, baldness and
CC	degenerative or traumatic disorders of the sensory epithelium of the
XX	inner ear
SQ	Sequence 728 AA;

Query Match		98.9%;	Score 4108;	DB 3;	Length 728;
Best Local Similarity		99.0%;	Pred. No. 2.6e-225;		
Matches 721;		Conservative	1;	Mismatches 6;	Indels 0; Gaps 0;
Qy	1	MGRFLLTLALLSALLCRQVDGSGVFELKLOEFVNKKGLLSNRNCRRGGPGGAGQOQC	60		
Db	1	MGRFLLTLALLSALLCRQVDGSGVFELKLOEFVNKKGLLSNRNCRRGGPGGAGQOQC	60		
Qy	61	DCKTFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSPDGAGADPAFNPTRFPFG	120		
Db	61	DCKTFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSPDGAGADPAFNPTRFPFG	120		
Qy	121	FTWPGTFSLLIEALHTDSPDDLTTENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY	180		
Db	121	FTWPGTFSLLIEALHTDSPDDLTTENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY	180		
Qy	181	SYRFVCDHEHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ	240		
Db	181	SYRFVCDHEHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ	240		
Qy	241	HGFCDPGECKRCRVWQGRYCDICIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYCT	300		
Db	241	HGFCDPGECKRCRVWQGRYCDICIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYCT	300		
Qy	301	HHKPCNGATCTNTGQGSVTCSCRPGYTCSSCEIENECDANPCNKGSGCTDLENSYCT	360		
Db	301	HHKPCNGATCTNTGQGSVTCSCRPGYTCSSCEIENECDANPCNKGSGCTDLENSYCT	360		
Qy	361	CPGFGYKNCELSAMTCADGPCFNGRCSDSPDGGYSCRCPLGYSGFNCCKIDYCSSSP	420		
Db	361	CPGFGYKNCELSAMTCADGPCFNGRCSDSPDGGYSCRCPLGYSGFNCCKIDYCSSSP	420		
Qy	421	CANGAQCVDLGNYSYICQOAGFTGRHCDNVDPCASFPCVNGGTCODGVNDYSCTCPGY	480		
Db	421	CANGAQCVDLGNYSYICQOAGFTGRHCDNVDPCASFPCVNGGTCODGVNDYSCTCPGY	480		
Qy	481	NGKNCSTPVSRCBHNCHNGATCHERSNRYVCECARGYGLNCQFLPPEPQGVIVDFT	540		
Db	481	NGKNCSTPVSRCBHNCHNGATCHERSNRYVCECARGYGLNCQFLPPEPQGVIVDFT	540		
Qy	541	EKYTEQNSQFPPIAVCAGIILVLLGCAATVVCRLKVRKHOPACHSETETMNN	600		
Db	541	EKYTEQNSQFPPIAVCAGIILVLLGCAATVVCRLKVRKHOPACHSETETMNN	600		
Qy	601	LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVVDYNLVHELKNEDSV	660		
Db	601	LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVVDYNLVHELKNEDSV	660		
Qy	661	KEEHGKCAKCTYDSEAEKSAVOLKSDTSERKEPDSVYSTKDYQSVYVISEEKD	720		
Db	661	KEEHGKCAKCTYDSEAEKSAVOLKSDTSERKEPDSVYSTKDYQSVYVISEEKD	720		
Qy	721	ECIIATEV 728			
Db	721	ECIIATEV 728			
RESULT 4					
AAW18353					
ID	AAW18353 standard; protein; 723 AA.				
XX	AAW18353;				
AC	AAW18353;				
XX	11-FEB-1998 (first entry)				
DT	Proliferation and differentiation suppression polypeptide.				
DE	Proliferation and differentiation suppression polypeptide.				
XX	Proliferation; differentiation; suppression; human; delta-1; serrate-1;				
KW	blood cell; neuron; leukaemia; malignant tumour; immunosuppression.				
XX	Homo sapiens.				
OS					
XX					
EH	Key	Location/Qualifiers			
FT	Peptide	1..21			
FT	Protein	/label= Signal			
FT		22..723			
FT		/label= Differentiation_suppression_protein			
XX	WO9719172-A1.				
XX	29-MAY-1997.				
XX	15-NOV-1996;	96WO-JP003356.			
XX	17-NOV-1995;	95JP-00299611.			
PR	30-NOV-1995;	95JP-00311811.			
XX	(ASAH) ASahi KASEI KOGYO KK.				
XX	Sakano S, Itoh A;				
XX	WPI: 1997-298110/27.				
DR	N-PSDB; AAT70174.				
XX	Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress				
PT	proliferation and differentiation of undifferentiated human blood cells.				
XX	Claim 15; Page 77-82; 114pp; Japanese.				
PS	The present sequence represents a polypeptide which suppresses				
CC	proliferation and differentiation of undifferentiated cells such as				
CC	neurons and blood cells. The polypeptide may be used for the prevention				
CC	and control of disorders involving undifferentiated cells, such as				
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.				
CC	after immunosuppression				
XX	Sequence 723 AA;				
SQ	Query Match	84.1%;	Score 3494.5;	DB 2;	Length 723;
	Best Local Similarity	83.3%;	Pred. No. 1.8e-190;	Indels 11;	Gaps 7;
	Matches 609;	Conservative	47;	Mismatches 64;	
Qy	1	MGRFLLTLALLSALLCRQVDGSGVFELKLOEFVNKKGLLSNRNCRRGGPGGAGQOQC	60		
Db	1	MGRFLLTLALLSALLCRQVDGSGVFELKLOEFVNKKGLLSNRNCRRGGPGGAGQOQC	60		
Qy	61	DCKTFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSPDGAGADPAFNPTRFPFG	120		
Db	55	ACRTFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSPDGAGADPAFNPTRFPFG	113		
Qy	121	FTWPGTFSLLIEALHTDSPDDLTTENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY	180		
Db	114	FTWPGTFSLLIEALHTDSPDDLTTENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY	173		
Qy	181	SYRFVCDHEHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ	240		
Db	174	SYRFVCDHEHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ	233		
Qy	241	HGFCDPGECKRCRVWQGRYCDICIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYCT	300		
Db	234	HGFCDPGECKRCRVWQGRYCDICIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYCT	293		
Qy	301	HHKPCNGATCTNTGQGSVTCSCRPGYTCSSCEIENECDANPCNKGSGCTDLENSYCT	360		
Db	294	HHKPCNGATCTNTGQGSVTCSCRPGYTCSSCEIENECDANPCNKGSGCTDLENSYCT	353		
Qy	361	CPGFGYKNCELSAMTCADGPCFNGRCSDSPDGGYSCRCPLGYSGFNCCKIDYCSSSP	420		
Db	354	CPGFGYKNCELSAMTCADGPCFNGRCSDSPDGGYSCRCPLGYSGFNCCKIDYCSSSP	413		
Qy	421	CANGAQCVDLGNYSYICQOAGFTGRHCDNVDPCASFPCVNGGTCODGVNDYSCTCPGY	480		
Db	414	CSNGAKCVLDGAYLCRCQAGFSGRHCDNVDPCASFPCVNGGTCODGVNDYSCTCPGY	473		
Qy	481	NGKNCSTPVSRCBHNCHNGATCHERSNRYVCECARGYGLNCQFLPPEPQGVIVDFT	540		

[illegible]

FT Modified-site /label= EGF-like_domain
 FT 328..334 /note= "N-myristoylation domain"
 FT Modified-site 340..346 /note= "N-myristoylation site"
 FT Modified-site 342..346 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 343..355 /note= "Asn and Asp hydroxylation site"
 FT Modified-site 344..348 /note= "Casein kinase II phosphorylation site"
 FT Domain 352..364 /label= EGF-like_domain
 FT Modified-site 369..373 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 378..384 /note= "N-myristoylation site"
 FT Modified-site 387..393 /note= "N-myristoylation site"
 FT Domain 391..403 /label= EGF-like_domain
 FT Modified-site 420..432 /note= "Asn and Asp hydroxylation site"
 FT Domain 429..441 /label= EGF-like_domain
 FT Modified-site 457..461 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 458..480 /label= Asn and Asp hydroxylation site
 FT Domain 467..479 /label= EGF-like_domain
 FT Modified-site 477..481 /note= "N-glycosylation site"
 FT Modified-site 483..487 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 495..499 /note= "Casein kinase II phosphorylation site"
 FT Domain 505..517 /label= EGF-like_domain
 FT Modified-site 512..518 /note= "N-myristoylation site"
 FT Domain 548..568 /label= Transmembrane_domain
 FT Binding-site 552..563 /label= Prokaryotic membrane lipoprotein lipid attachment site
 FT Modified-site 659..663 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 660..664 /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
 FT Modified-site 670..674 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 671..675 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 676..682 /note= "N-myristoylation site"
 FT Modified-site 683..689 /note= "N-myristoylation site"
 FT Modified-site 695..701 /note= "N-myristoylation site"
 FT Modified-site 698..702 /note= "Casein kinase II phosphorylation site"
 FT W0200021996-A2.
 FT 20-APR-2000.
 FT 05-OCT-1999; 99WO-US023089.
 FT 13-OCT-1998; 98US-0104080P.
 FT (GETH) GENENTECH INC.

XX Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI;
 PI Yuan J;
 XX WPI; 2000-317943/27.
 DR N-PSDB; AAZ93703.
 XX Composition for inhibiting neoplastic cell growth and treating cancers of
 FT ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
 FT PRO538, PRO172 or PRO182 polypeptide or their agonist.
 XX Claim 12; Fig 8; 122pp; English.
 XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
 CC polypeptide or their agonists, mixed with a carrier is useful for
 CC inhibiting neoplastic growth and treating tumors such as cancers of
 CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
 CC central nervous system, melanoma and leukaemia
 XX Sequence 723 AA;
 SQ

Query Match 84.1%; Score 3494.5; DB 3; Length 723;
 Best Local Similarity 83.3%; Pred. No. 1.8e-190;
 Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;
 Qy 1 MGRFLTLTALLSALLCRCQVDSGVFELKQLQEFVNKKGLISNRNCRGGGPGGAGQOQC 60
 Db 1 MGRSALALAVLSALL--CQWSSGVFELKQLQEFVNKKGLGNRNCR---GGAGPPPC 54
 Qy 61 DCKTFFRVCLKHQOASVSPPTCTYGSATIPVLGANSFVDPDAGGADAPAPNIRPPFG 120
 Db 55 ACRTFFRVCLKHQOASVSPPTCTYGSATIPVLGANSFVDPDAGGADAPAPNIRPPFG 113
 Qy 121 FTWPGTFLIIEALHTDSPDILTENPERLISRLATORHLAVGEWSODLHSSGRTDLKY 180
 Db 114 FTWPGTFLIIEALHTDSPDILTENPERLISRLATORHLAVGEWSODLHSSGRTDLKY 173
 Qy 181 SYRFVCDHYHVGSCSVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDEQ 240
 Db 174 SYRFVCDHYHVGSCSVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDEQ 233
 Qy 241 HGFCDKPGCKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGHWGLFCNODLNYCT 300
 Db 234 HGFCDKPGCKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGHWGLFCNODLNYCT 293
 Qy 301 HHKPCNKGATCTNTGGSYTCSCRPGYTGSSCEIENECDANPCNKGSCSTDLENSYCT 360
 Db 294 HHKPCNKGATCTNTGGSYTCSCRPGYTGATCELGIDECDPSPCKNGSCSTDLENSYCT 353
 Qy 361 CPPGFGKNCSELSAMTCADGFCFNGGRCTDNPDGGYSCRCPLGYSGFNCCKIDYCS SSP 420
 Db 354 CPPGFGKICELSAMTCADGFCFNGGRCTDNPDGGYSCRCPLGYSGFNCCKIDYCS SSP 413
 Qy 421 CANGAQCVDLGSNYICOCQAGTGRHCDNDVDDCASFPVCVNGGTCCQGVNDYSCTCPGY 480
 Db 414 CSNGAKCVDLGDAYLCRCQAGTGRHCDNDVDDCASFPVCVNGGTCCQGVNDYSCTCPGY 473
 Qy 481 NGKNCSTPVSRCHEHNCNGATCHERSNRVVCSCARGYGLNCOFLPPEPGPIVDFT 540
 Db 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVBCARGYGGPNCOFLPPEPGPIVDFT 533
 Qy 541 EKYTEGQNSOPPIAVCAGIILVLMILLGCAAVVVCVRLKVKQRHHQPEACRSSETMNN 600
 Db 534 EK-LEGQGGFFPWAVVAVCAGIILVLMILLGCAAVVVCVRLKVKQRHHQPEACRSSETMNN 592
 Qy 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKRYPSVDYVNLVHKLKNE- 658
 Db 593 LANCQREKDISISVIGATQIKNTNKKADPHGDSADKNGFKARYPAVDYVNLVODLKGDDT 652
 Qy 659 SVKEEHGCKEAKCETVDSAEK-SAVOLKSSDTSEKRPDSVYSTSKDTKYOSVYVISE 717
 Db 653 AVRAHSHKRDTCQPOGSGSEKGTPTTLRGGEASERKRPDSGCSSTKDTKYOSVYVISE 712

QY 718 EKDECIATEV 728
Db 713 EKDECIATEV 723

RESULT 8
ID AAB33422
AC AAB33422; standard; protein; 723 AA.
XX AAB33422;
XX 29-JAN-2001 (first entry)
XX Human PRO172 protein UNQ146 SEQ ID NO:41.
DE
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028304.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000216.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI: 2000-572271/53.
DR N-PSDB; AAC58587.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 33; Fig 18; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 723 AA;
Query Match 84.1%; Score 3494.5; DB 3; Length 723;
Best Local Similarity 83.3%; Pred. No. 1.8e-190; Mismatches 64; Indels 11; Gaps 7;
Matches 609; Conservative 47;
QY 1 MGRFLTLALISALLCQCQVDGSGVFELKQEFVYKKGKLLSNRNCRCGGGPGGAGQQQC 60
Db 1 MGRCALALAVLSALL--CQWSSGVFELKQEFVYKKGKLLGNRNCRC---GGAGPPPC 54
QY 61 DKTFFRVCLKHQYQASVSPPEPTTYSATITPVLGANSFVSDPGAGADPAFNPTRFPFG 120
Db 55 ACRTFFRVCLKHQYQASVSPPEPTTYSATITPVLGVDVDFSLPDG--GGADSAFNPTRFPFG 113
QY 121 FTWPGTFSLLIHALHTDSPDDLTTENPERLSRLATQRHLAVGEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFSLLIHALHTDSPDDLATENPERLSRLATQRHLTVGEWSQDLHSSGRTDLKY 173
QY 181 SYRFVCDHYHYGEGCSVFCRPRDRFGHFTCGERKVCNCPQWQCQBGWGLFCNQDLNYCT 240
Db 174 SYRFVCDHYHYGEGCSVFCRPRDDAFGHFTCGERKVCNCPQWKGFPCTEPLCLPGCDSQ 233
QY 241 HGFCDKPGCKRVGWQGRYCDCEIRYFGCLHGTCCQWQCQBGWGLFCNQDLNYCT 300
Db 234 HGFCDKPGCKRVGWQGRYCDCEIRYFGCLHGTCCQWQCQBGWGLFCNQDLNYCT 293
QY 301 HHKPKNGATCNTTQGSYVTCSCRPGYTGSSCEIINECDANPCKNGSGCTDLENSYCT 360
Db 294 HHKPKNGATCNTTQGSYVTCSCRPGYTGATCELGIDECIDPSPCKNGSGCTDLENSYCT 353
QY 361 CPPGFYGNCELSAMTADGFCFNGRCRTNDPDGYSRCRPLGYSGFNCEKIDYCSSSP 420
Db 354 CPPGFYGIKCELSAMTADGFCFNGRCSDSPDGGYSCRCPPVGYSGFNCEKIDYCSSSP 413

XX	(GETH) GENENTECH INC.	
XX	Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;	
XX	Yuan J;	
XX	WPI; 2000-638201/61.	
XX	N-PSDB; AAAS4105.	
XX	PRO211, PRO228, PRO338, PRO172 and PRO182 polypeptides useful for	
XX	treating tumors including cancers of the breast and lung, leukemia and	
XX	for identifying compounds capable of inhibiting growth of neoplastic	
XX	cells.	
XX	Claim 31; Fig 8; 133pp; English.	
XX	Isolated PRO211, PRO228, PRO338, PRO172 or PRO182 polypeptides or their	
XX	agonists (preferably anti-PRO agonist antibody or a small molecule	
XX	mimicking the biological activity of PRO polypeptide) are useful in vitro	
XX	or in vivo for inhibiting the growth of a tumour cell. Compositions	
XX	comprising the PRO polypeptides are useful for inhibiting neoplastic cell	
XX	growth and for treating cancer including breast, ovarian, renal,	
XX	colorectal, uterine, prostate, lung, bladder, central nervous system	
XX	cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also	
XX	useful for treating other disorders such as neuronal, glial, astrocytal,	
XX	hypothalamic and other glandular, macrophagal, epithelial, stromal,	
XX	blastocoealic disorders and inflammatory, angiogenic and immunologic	
XX	disorders as well as being useful for identifying agonists to PRO	
XX	polypeptides by contacting the polypeptide with a candidate molecule and	
XX	monitoring biological activity mediated by the polypeptide	
XX	Sequence 723 AA;	
XX	Query Match 84.1%; Score 3494.5; DB 3; Length 723;	
XX	Best Local Similarity 83.3%; Pred. No. 1.8e-190;	
XX	Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;	
Qy	1 MGRFLTLTALLSALLCRQVDGSGVFELKQEFVNKKGLLSNRNCCRGGGGFGAGQQQC 60	
Db	1 MGRSCALALAVLSALL--CQWSSGVFELKQEFVNKKGLLGNRCCR---GGAGPPPC 54	
Qy	61 DCKTFFRVCLKHQASVSPPCPTGSAITPVLGANSFSDGAGGADPAPSNIRPFG 120	
Db	55 ACRTFFRVCLKHQASVSPPCPTGSAITPVLGANSFSDGAGGADPAPSNIRPFG 113	
Qy	121 FTWPGTSLIEALHTSDPDLTTENPERLSRLATRHLAGVSEWSDLHSSGRTDLKY 180	
Db	114 FTWPGTSLIEALHTSDPDLTATENPERLSRLATRHLAGVSEWSDLHSSGRTDLKY 173	
Qy	181 SYRFVCDHEHYGEGSVFCRPRDRDFGHFTCGERGEKVCNPGWGOYCTEPICLPGCDEQ 240	
Db	174 SYRFVCDHEHYGEGSVFCRPRDDAFGHFTCGERGEKVCNPGWGPYCTEPICLPGCDEQ 233	
Qy	241 HGFCDKFGCKRCRVGMOGRYDCIRYPGCLHGTCCQPMQCNQEGWGLFCNQDLNYCT 300	
Db	234 HGFCDKFGCKRCRVGMOGRYDCIRYPGCLHGTCCQPMQCNQEGWGLFCNQDLNYCT 293	
Qy	301 HHKCKNGATCTNNGSGYTCSCRPYTGSSCETIEINECDANPCNKGSCGTDLENSYCT 360	
Db	294 HHKCKNGATCTNNGSGYTCSCRPYTGATCELGIDECPSPCNKGSCGTDLENSYCT 353	
Qy	361 CPPGFGKNCNELSANTCADGPCFNGRCRTNPDGGYSCRCPLGYSGFNCCKIDYCS SSP 420	
Db	354 CPPGFGKICELSAANTCADGPCFNGRCSDSPDGYSCRCPCPVGYSGFNCCKIDYCS SSP 413	
Qy	421 CANGAQCVDLGNSYICQCAQAGTCRHCDDNVDDCASFPVNGGTCQDGVNDYSCCTCPGY 480	
Db	414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRQGVNDFSCCTCPGY 473	
Qy	481 NGKNCSTPVSRCEHNPCHNGATCHERNYVCECARGYGLNCFLLPPEPGVVDFT 540	
Db	474 TGRNCSPVSRCEHNPCHNGATCHERHRYVCECARGYGGPNCFLLPELPPGPAVVDLT 533	
Qy	541 EKYTEGQNSQFPMTAVACAGIILVLLMLLGGCAAIVVCLRVLRKVQKRHHQPEACRSETETWNN 600	
Db	534 EK-LEGQGGPMPVAVCAGVILVLLMLLGGCAAIVVCLRVLRQKRRPPADPCRGETETWNN 592	
Qy	601 LANCOREKDISISVIGATQIKNTNKKVDVFDHSDNS-DKNGYKVRYPVDYNLAVHELKNEP- 658	
Db	593 LANCOREKDISVSIIGATQIKNTNKKADFDHSDNSADKNGFKARYPAVDYNLVQDLKGGDT 652	
Qy	659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPSDVYSTSKDTKYQSVYVISE 717	
Db	653 AVRDASHKRDTCOPQGSSEGEKGTPTTLRGGEASERKRPSDGGCSTSKDTKYQSVYVISE 712	
Qy	718 EKDECIATEV 728	
Db	713 EKDECVIATEV 723	
XX	RESULT 11	
XX	AAU12344	
XX	ID AAU12344 standard; protein; 723 AA.	
XX	AC AAU12344;	
XX	XX 24-OCT-2001 (first entry)	
XX	XX Human PRO172 polypeptide sequence.	
XX	XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;	
XX	XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;	
XX	XX ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;	
XX	XX A-peptide; factor VIIA; gene therapy.	
XX	XX Homo sapiens.	
XX	XX WO200140466-A2.	
XX	XX 07-JUN-2001.	
XX	XX 01-DEC-2000; 2000WO-US032678.	
XX	XX 01-DEC-1999; 99WO-US028301.	
XX	XX 01-DEC-1999; 99WO-US028634.	
XX	XX 02-DEC-1999; 99WO-US028551.	
XX	XX 02-DEC-1999; 99WO-US028564.	
XX	XX 02-DEC-1999; 99WO-US028565.	
XX	XX 09-DEC-1999; 99US-0170262P.	
XX	XX 16-DEC-1999; 99WO-US030095.	
XX	XX 20-DEC-1999; 99WO-US030911.	
XX	XX 20-DEC-1999; 99WO-US030999.	
XX	XX 30-DEC-1999; 99WO-US031243.	
XX	XX 30-DEC-1999; 99WO-US031274.	
XX	XX 05-JAN-2000; 2000WO-US000219.	
XX	XX 06-JAN-2000; 2000WO-US000277.	
XX	XX 06-JAN-2000; 2000WO-US000376.	
XX	XX 11-FEB-2000; 2000WO-US003565.	
XX	XX 18-FEB-2000; 2000WO-US000431.	
XX	XX 18-FEB-2000; 2000WO-US004342.	
XX	XX 22-FEB-2000; 2000WO-US004414.	
XX	XX 24-FEB-2000; 2000WO-US004914.	
XX	XX 24-FEB-2000; 2000WO-US005004.	
XX	XX 01-MAR-2000; 2000WO-US005601.	
XX	XX 02-MAR-2000; 2000WO-US005841.	
XX	XX 03-MAR-2000; 2000US-0187202P.	
XX	XX 10-MAR-2000; 2000WO-US006319.	
XX	XX 13-MAR-2000; 2000WO-US006884.	
XX	XX 20-MAR-2000; 2000WO-US007377.	
XX	XX 21-MAR-2000; 2000WO-US007532.	
XX	XX 30-MAR-2000; 2000WO-US008439.	
XX	XX 17-MAY-2000; 2000WO-US013705.	
XX	XX 22-MAY-2000; 2000WO-US014042.	
XX	XX 30-MAY-2000; 2000WO-US014941.	
XX	XX 02-JUN-2000; 2000WO-US015264.	
XX	XX 05-JUN-2000; 2000US-0209832P.	

PR	28-JUL-2000;	2000WO-US020710.	
PR	11-AUG-2000;	2000WO-US022031.	
PR	23-AUG-2000;	2000WO-US023522.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	08-NOV-2000;	2000WO-US030952.	
PR	10-NOV-2000;	2000WO-US030873.	
XX	(GETH)	GENENTECH INC.	
XX			
PI	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;		
PI	Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;		
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;		
XX			
DR	WPI: 2001-408281/43.		
DR	N-PSDB; AAS21416.		
XX			
PT	Isolated , secretory and transmembrane PRO polypeptide used to detect		
PT	other PRO polypeptides, link bioactive molecules to cells expressing PRO		
PT	polypeptides, and detect the presence of mammalian tumors e.g. lung,		
PT	breast, prostate, cervical.		
XX			
PS	Claim 12; Fig 346; 813pp; English.		
XX			
CC	AAU12172-AAU12446 represent novel human secretory and transmembrane PRO		
CC	polypeptides. The PRO polypeptides are useful to detect other PRO		
CC	polypeptides, to link bioactive molecules to cells expressing PRO		
CC	polypeptides, to modulate biological activities of cells expressing PRO		
CC	polypeptides, and to detect the presence of mammalian lung, colon,		
CC	breast, prostate, rectal, cervical or liver tumours by comparing PRO		
CC	polypeptide expression in a cell sample to that in a control sample. Some		
CC	of the 275 sequences are also useful to stimulate the release of tumour		
CC	necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or		
CC	differentiation of chondrocytes, the proliferation or gene expression in		
CC	pericyte cells, the release of proteoglycans from cartilage, the		
CC	proliferation of inner ear utricular supporting cells or of T-		
CC	lymphocytes, the release of a cytokine from peripheral blood monocytes		
CC	(PBMCs), or the proliferation of endothelial cells. Some of the PRO		
CC	polypeptides may modulate glucose or free fatty acid uptake by skeletal		
CC	muscle cells or by adipocytes; or inhibit binding of A-peptide to factor		
CC	VIIIA. The PRO polypeptides can be used in assays to identify molecules		
CC	involved in binding interactions. The polynucleotides encoding PRO		
CC	polypeptides can be used to generate probes, antisense RNA/DNA,		
CC	transgenic or knock out animals and can be used in gene therapy		
XX			
SQ	Sequence 723 AA;		
Query Match			
Best Local Similarity 83.3%; Pred. NO. 1.8e-190;			
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;			
QY	1	MGRFLLTLALISALLCRQVDGSGVFELKLOEFVNKKGLLSNRNCCRGGGGAGQQQC	60
DB	1	MGRFCALAVLSALL--CQWSSGVFELKLOEFVNKKGLLGNRCR---GGAGPPPC	54
QY	61	DCKTFPRVCLKHYQASVSEPPCTGYSAITPVLGANSFSPVDCGAGDPAFNPTRFPFG	120
DB	55	ACRTFPRVCLKHYQASVSEPPCTGYSAITPVLGVSFSLPDG--GGADSAFNPTRFPFG	113
QY	121	FTWPGTFLIIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY	180
DB	114	FTWPGTFLIIIEALHTDSPDDLTTENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKY	173
QY	181	SYRFVDEHYHGGCVSFRCPRDDRGHTTCGERGEKVCNPGWKGYCTEPTCLPGCDRQ	240
DB	174	SYRFVDEHYHGGCVSFRCPRDDRGHTTCGERGEKVCNPGWKGYCTEPTCLPGCDRQ	233
QY	241	HGFCDKPGCKRQVWQGYCDECIYRPGCLHGTCTQCPQWQCOCQEGWGLFCNQDLNYCT	300
DB	234	HGFCDKPGCKRQVWQGYCDECIYRPGCLHGTCTQCPQWQCOCQEGWGLFCNQDLNYCT	293
QY	301	HHKPKCKNGATCTNTGGSYTCSCRPGYTGSSCBIEINECDANPKCKNGSGCTDLNSYSCT	360
DB	294	HHKPKCKNGATCTNTGGSYTCSCRPGYTGATCELGLIDECDDPSCKNGSGCTDLNSYSCT	353
RESULT 12			
AAB53064			
ID	AAB53064	standard; protein; 723 AA.	
AC	AAB53064;		
DT	28-FEB-2001	(first entry)	
XX			
DE	Human angiogenesis-associated protein PRO172, SEQ ID NO:2.		
XX			
KW	Human; angiogenesis-associated protein; PRO; endothelial cell growth;		
KW	cardiac hypertrophy; cardiovascular disorder; endothelial disorder;		
KW	angiogenic disorder; atherosclerosis; osteoporosis; hypertension;		
KW	myocardial infarction; diabetic retinopathy; rheumatoid arthritis;		
KW	Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;		
KW	Alzheimer's disease; Huntington's disease; stroke; drug screening;		
XX	gene therapy; transgenic animal.		
OS	Homo sapiens.		
PN	WO2000053753-A2.		
XX			
PD	14-SEP-2000.		
XX			
PF	05-JAN-2000; 2000WO-US000219.		
PR	08-MAR-1999; 99WO-US005028.		
PR	12-MAR-1999; 99US-0123957P.		
PR	14-MAY-1999; 99US-0134287P.		
PR	02-JUN-1999; 99WO-US012252.		
PR	23-JUN-1999; 99US-0141037P.		
PR	20-JUL-1999; 99US-0144758P.		
PR	26-JUL-1999; 99US-0145698P.		
PR	01-SEP-1999; 99WO-US020111.		
PR	08-SEP-1999; 99WO-US020594.		
PR	15-SEP-1999; 99WO-US021090.		
PR	05-SEP-1999; 99WO-US021547.		
PR	05-OCT-1999; 99WO-US023089.		
PR	30-NOV-1999; 99WO-US028313.		
PR	30-NOV-1999; 99WO-US028409.		
PR	02-DEC-1999; 99WO-US028564.		
XX	02-DEC-1999; 99WO-US028565.		


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PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US003076.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006684.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.

PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Geritsaen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-341980/32.
XX N-PSDB; ACD24025.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
XX Claim 12; Fig 346; 660pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, or inhibit
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
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XX Sequence 723 AA;
Query Match 84.1%; Score 3494.5; DB 6; Length 723;
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XX 23-JUN-2003 (first entry)
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KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
KW antidiabetic; anorectic; vulnary; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
XX OS Homo sapiens.
XX XX
XX FN US2003004311-A1.
XX XX
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PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
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PR 13-SEP-1999; 99WO-US020944.
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Job time : 86.5563 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:26:20 ; Search time 73.3366 Seconds
(without alignments)
3520.994 Million cell updates/sec

Title: US-09-783-931-2

Perfect score: 4153

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	3495.5	84.2	721	10	US-09-783-931-5
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ALIGNMENTS

RESULT 1

US-09-908-322-2
; Sequence 2, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908.322

FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: 08/981.392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-908-322-2

Query Match 100.0%; Score 4153; DB 9; Length 728;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 2, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: I8n-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Taakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
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US-09-783-931-2

Query Match 100.0%; Score 4153; DB 10; Length 728;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 CANGAQCVDLGNSYICQCAQAGTGRHCDNDVDDCASFFCVNGGTCCDGVNDYSCTCPGY 480
Qy 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPOGPVIVDFT 540
Db 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPOGPVIVDFT 540
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLLGCAAIWCVRLKVQRHHQPEACRSETETWNN 600
Db 541 EKYTEGQNSQFPWIAVCAGIILVLLGCAAIWCVRLKVQRHHQPEACRSETETWNN 600
Qy 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVSDYNLHVELKNEDSV 660
Db 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVSDYNLHVELKNEDSV 660
Qy 661 KEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEBK 720
Db 661 KEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEBK 720
Qy 721 ECIATEV 728
Db 721 ECIATEV 728

RESULT 3
US-10-417-719-8
; Sequence 8, Application US/1041719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT APPLICATION NUMBER: US/10/417,719
; CURRENT FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 08/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Gallus Gallus
US-10-417-719-8

Query Match 99.7%; Score 4142.5; DB 14; Length 729;
Best Local Similarity 99.9%; Pred. No. 1.5e-265;
Matches 728; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MGRFLITLALLSALLCRQVDGSGVFELKQEFVFNKKGLLSNRNCRCGGGPGGAGQOQC 60
Db 1 MGRFLITLALLSALLCRQVDGSGVFELKQEFVFNKKGLLSNRNCRCGGGPGGAGQOQC 60
Qy 61 DCKTFFRVCLKHQASVSPPECTYGSAITPVLGANSFVDPGAGGADPAFNPFRPFG 120
Db 61 DCKTFFRVCLKHQASVSPPECTYGSAITPVLGANSFVDPGAGGADPAFNPFRPFG 120
Qy 121 FTWGTSLIIEALHTSDPDLTTENPERLISRLATQORHLAVGEWSODLHSSGRTDLKY 180
Db 121 FTWGTSLIIEALHTSDPDLTTENPERLISRLATQORHLAVGEWSODLHSSGRTDLKY 180

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Qy 181 SYRFVCDHEHYGEGSVFCRPRDRDFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDBQ 240
Db 181 SYRFVCDHEHYGEGSVFCRPRDRDFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDBQ 240
Qy 241 HGFCDKPECKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWSGLFCNQDLNCT 300
Db 241 HGFCDKPECKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWSGLFCNQDLNCT 300
Qy 301 HHKPKNGATCTNTGGSYTCSCRFYTGSSCEIENECDANPCKNKGSCDTLENSYCT 360
Db 301 HHKPKNGATCTNTGGSYTCSCRFYTGSSCEIENECDANPCKNKGSCDTLENSYCT 360
Qy 361 CPPGYGKNCESAMTADGPGCFNGGRCCTDNDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420
Db 361 CPPGYGKNCESAMTADGPGCFNGGRCCTDNDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420
Qy 421 CANGAQCVDLGNSYICQCAQAGTGRHCDNDVDDCASFFCVNGGTCCDGVNDYSCTCPGY 480
Db 421 CANGAQCVDLGNSYICQCAQAGTGRHCDNDVDDCASFFCVNGGTCCDGVNDYSCTCPGY 480
Qy 480 YNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPOGPVIVDF 539
Db 481 YNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPOGPVIVDF 540
Qy 540 TEKYTEGQNSQFPWIAVCAGIILVLLGCAAIWCVRLKVQRHHQPEACRSETETWNN 599
Db 541 TEKYTEGQNSQFPWIAVCAGIILVLLGCAAIWCVRLKVQRHHQPEACRSETETWNN 600
Qy 600 NLANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVSDYNLHVELKNEDS 659
Db 601 NLANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVSDYNLHVELKNEDS 660
Qy 660 VKEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEK 719
Db 661 VKEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEK 720
Qy 720 ECIATEV 728
Db 721 ECIATEV 728

RESULT 4
US-09-908-322-5
; Sequence 5, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392

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FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
Query Match 84.2%; Score 3495.5; DB 9; Length 721;
Best Local Similarity 82.2%; Pred. No. 9e-223;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;
QY 1 MGRFLLTLALLSALLCRQVDSGVFELKLOEFVNKGLLSNRNCCRGGPGG-AGQOO 59
DB 1 MGQORMLTLLVLSAVL--CQISCSGLFELRLQEFVNKGLLGNMCCR---PGSLASLOR 55
QY 60 CDCKTFRVCLKHQYASVSPPECTYGSATPTVLGANSFSPDAGAGADPAFSPNIRPFP 119
DB 56 CECKTFRICLKHQYNSVSPPECTYGGAVTPVLGTNSFVWPE-SSNADPTFSNIRPFP 114
QY 120 GFTWPGTFSLLIEALHTDSPDLTTENPERLLSRLATQRLHLAGVEWSODLHSSGRTDLK 179
DB 115 GFTWPGTFSLLIEAHADSADDLNTENPERLLSRLATQRLHLAGVEWSODLHSSGRTDLK 174
QY 180 YSYRFVCDHYHGGCVSFCRPRDRFHFCTGGERGKVCNPGWKGQYCTEPICLPGCDE 239
DB 175 YSYRFVCDHYHGGCVSFCRPRDRFHFCTGGERGKVCNPGWKGQYCTEPICLPGCDE 234
QY 240 QHGFCDKPGCKRVQWQGRYDECIRYPCGLHGTCCQPMQNCQBGWGLFCNQDLNYC 299
DB 235 HHGYCDKPGCKRVQWQGRYDECIRYPCGLHGTCCQPMQNCQBGWGLFCNQDLNYC 294
QY 300 THHKPCNGATCNTGGSTYCSRGYTCSSCEIENSCDANPCKNNGSCSDLENSYTC 359
DB 295 THHKPCNGATCNTGGSTYCSRGYTCSSCEIENSCDANPCKNNGSCSDLENSYTC 354
QY 360 TCPPFGYKNCCLSAAMTCADGPCFNGGRCTDNDPGGYSCRCPLGYSGFNCCKIDYCSS 419
DB 355 SCLPPFGYKNCCLSAAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCCKIDYCSS 414
QY 420 PCANGACQVDLGNYSYTCQQAQGTGRHCDNDVDDCASFPFCVNGGTCCQGVNDYSCTCPPG 479
DB 415 PCANGARCEDLGNYSYTCQQAQGTGRHCDNDVDDCASFPFCVNGGTCCQGVNDYSCTCPPG 474
QY 480 YNKNKCSPTVSRCEHPNCHNGATCHERSNRYVCECARGYGGNLCQFLLEPPQGPVINDF 539
DB 475 YIGKNCSPMTTKCEHPNCHNGATCHERNRYVCCARGYGGNLCQFLLEPPQGPVINDF 532
QY 540 TEKYTEGQNSQFWIAVACAGIILVLLGLCAAIVVCLVKVKRHHQPEACRSETETWN 599
DB 533 TEKYTEGQNSQFWIAVACAGIILVLLGLCAAIVVCLVKVKRHHQPEACRSETETWN 592
QY 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSD-NSDKNGYKVRYPVSYNVLVHELKNE 658
DB 593 NLANCQREKDISISVIGATQIKNTNKKIDFLSNNKNGYKVRYPVSYNVLVHELKNE 652
QY 659 SVKEEHGKCEAKETVDSAEKSAVOLKSSDTSERKRDSDVSTSKDTKYQSYVYVISE 718
DB 653 SPKEERKCEAKCSSDSDSDVNSVHSK-RDSSERRRDPDSYSTSKDTKYQSYVYVISE 711
QY 719 KDECIATEV 728
|||||

712 KDECIATEV 721
RESULT 5
US-09-783-931-5
; Sequence 5, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Teakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Autler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-783-931-5
Query Match 84.2%; Score 3495.5; DB 10; Length 721;
Best Local Similarity 82.2%; Pred. No. 9e-223;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;
QY 1 MGRFLLTLALLSALLCRQVDSGVFELKLOEFVNKGLLSNRNCCRGGPGG-AGQOO 59
DB 1 MGQORMLTLLVLSAVL--CQISCSGLFELRLQEFVNKGLLGNMCCR---PGSLASLOR 55
QY 60 CDCKTFRVCLKHQYASVSPPECTYGSATPTVLGANSFSPDAGAGADPAFSPNIRPFP 119
DB 56 CECKTFRICLKHQYNSVSPPECTYGGAVTPVLGTNSFVWPE-SSNADPTFSNIRPFP 114
QY 120 GFTWPGTFSLLIEALHTDSPDLTTENPERLLSRLATQRLHLAGVEWSODLHSSGRTDLK 179
DB 115 GFTWPGTFSLLIEAHADSADDLNTENPERLLSRLATQRLHLAGVEWSODLHSSGRTDLK 174
QY 180 YSYRFVCDHYHGGCVSFCRPRDRFHFCTGGERGKVCNPGWKGQYCTEPICLPGCDE 239
DB 175 YSYRFVCDHYHGGCVSFCRPRDRFHFCTGGERGKVCNPGWKGQYCTEPICLPGCDE 234

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Qy 240 QHGFCDKPGCKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCGMGGGLFCNQDLNYC 299
Db 235 HHGYCDKPGCKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCGMGGGLFCNQDLNYC 294
Qy 300 THHKPCKNAGTCTNTGQSYTCSCRPVGTGSSCEIEINECDANPKNGSGCTDLNYSVC 359
Db 295 THHKPCENGATCTNTGQSYTCSCRPVGTGSSCEIEINECDANPKNGSGCTDLNYSVC 354
Qy 360 TCPGFGYGNKCELSAMTADGPCFNGGRCTDNPDGYSRCPLGYSGFNCCKKIDYCSSS 419
Db 355 SCPPGFGYGNKCELSAMTADGPCFNGGRCADNPDGGYICFCPVGYSGFNCCKKIDYCSSN 414
Qy 420 PCANGAQCVDLGNSYICQCGAGTGRHCDNDVDCASFPVNGGTCQDGVNDYSCCTCPPG 479
Db 415 PCANGARCEDLGNSYICQCGAGTGRHCDNDVDCASFPVNGGTCQDGVNDYSCCTCPPG 474
Qy 480 YNGKNCSTPVSRCENHPCHNGATCHERNRNVYVCECARGYGLNQCFLPPQGPVIVDF 539
Db 475 YIGKNCSPITTKCHNPCHNGATCHERNRNVYVCECARGYGLNQCFLPPG--EKPVVVDL 532
Qy 540 TEKYTEGONSOPFWIAVCAGIILVLLGLCAAIVCVRLKVQRHHQPEACRSETETMN 599
Db 533 TEKYTEGONSOPFWIAVCAGIILVLLGLCAAIVCVRLKVQRHHQPEACRSETETMN 592
Qy 600 NLANCQREKDISISVIGATQIKNTNKKYDFHSD--NSDKNGYKVRYPVSDYVNLVHELKNE 658
Db 593 NLANCQREKDISISVIGATQIKNTNKKIDFLSESNNEKNGYKVRYPVSDYVNLVHELKNE 652
Qy 659 SVKEEHGKCEAKCETVDSAEBSAQLKSSDTSERKRPDPSVYSTKDTKYQSVYVISEE 718
Db 653 SPKEERSKCEAKGSSNDSDESVNSVHSK--RDSERRRRPDSAYSTSKDTKYQSVYVISE 711
Qy 719 KDECIATEV 728
Db 712 KDECIATEV 721
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RESULT 6

US-10-042-865-109
Sequence 109, Application US/10042865

Publication No. US20040029216A1

GENERAL INFORMATION:

APPLICANT: Padigaru, Muralidhara

APPLICANT: Li, Li

APPLICANT: Zerhusen, Bryan D

APPLICANT: Casman, Stacie J

APPLICANT: Shenoy, Suresh G

APPLICANT: Spytek, Kimberly

APPLICANT: Zhong, Mei

APPLICANT: Gangolli, Esha A

APPLICANT: Burgess, Catherine E

APPLICANT: Patturajan, Meera

APPLICANT: Vernet, Corine A.M

APPLICANT: Taylor, Sarah

APPLICANT: Tchernev, Velizar T

APPLICANT: Miller, Charles E

APPLICANT: Guo, Xiaojia

APPLICANT: Boldog, Ference L

APPLICANT: Grosse, William M

APPLICANT: Alsebrook II, John P

APPLICANT: Gerlach, Valerie L

APPLICANT: Edinger, Shlomit R

APPLICANT: Rothenberg, Mark E

APPLICANT: Ellerman, Karen

APPLICANT: MacDougall, John

APPLICANT: Malyankar, Uriel M

APPLICANT: Millet, Isabelle

APPLICANT: Peyman, John

APPLICANT: Smithson, Glenna

APPLICANT: Gunther, Erik

APPLICANT: Stone, David

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

TITLE OF INVENTION: Using the Same

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; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042.865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-042-865-109
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Query Match

Best Local Similarity 84.2%; Score 3495.5; DB 15; Length 721;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;

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Qy 1 MGRFLLTALLSALLCRCQVDSGVFELKLOEFVNKKGLLSNRNCRGGGPGG-AGOOQ 59
Db 1 MGQRMULTLVLNSAVL--CQISCSGLFELRLOEFVNKKGLGNWCCR---PGLSLAQ 55
Qy 60 CDCKTFPRVCLKHQYASVSPPECTYGSATPVLGANSFVSPDGAGGADPAFSPNRP 119
Db 56 CECKTFPRICLKHQYNSVSPPECTYGCATPVLTGNSFVVPE--SSNADTFSPNRP 114
Qy 120 GFTWPGTFSLIIEALHTDSDDLTETENPERLISLATORHLAVGEESQDLHSSRDT 179
Db 115 GFTWPGTFSLIIEAHADSADLNTENPERLISLATORHLTVGEQSWQDLHSSRDT 174
Qy 180 YSYRFVCDHYGEGCSVFCRPRDDRFGHTFCGGRGKVCNPGMKGOYCTEPICLPG 239
Db 175 YSYRFVCDHYGEGCSVFCRPRDDAFGHFSGEKGKLCNPGMKGLYCTEPICLPG 234
Qy 240 QHGFCDKPGCKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCGMGGGLFC 299
Db 235 HHGYCDKPGCKRCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCGMGGGLFC 294
Qy 300 THHKPCKNAGTCTNTGQSYTCSCRPVGTGSSCEIEINECDANPKNGSGCTDLN 359
Db 295 THHKPCENGATCTNTGQSYTCSCRPVGTGSSCEIEINECDANPKNGSGCTDLN 354
Qy 360 TCPGFGYGNKCELSAMTADGPCFNGGRCTDNPDGYSRCPLGYSGFNCCKKIDYCS 419
Db 355 SCPPGFGYGNKCELSAMTADGPCFNGGRCADNPDGGYICFCPVGYSGFNCCKK 414
Qy 420 PCANGAQCVDLGNSYICQCGAGTGRHCDNDVDCASFPVNGGTCQDGVNDYSC 479
Db 415 PCANGARCEDLGNSYICQCGAGTGRHCDNDVDCASFPVNGGTCQDGVNDYSC 474
Qy 480 YNGKNCSTPVSRCENHPCHNGATCHERNRNVYVCECARGYGLNQCFLPPQGP 539
Db 475 YIGKNCSPITTKCHNPCHNGATCHERNRNVYVCECARGYGLNQCFLPPG--E 532
Qy 540 TEKYTEGONSOPFWIAVCAGIILVLLGLCAAIVCVRLKVQRHHQPEACRSETET 599
Db 533 TEKYTEGONSOPFWIAVCAGIILVLLGLCAAIVCVRLKVQRHHQPEACRSETET 592
Qy 600 NLANCQREKDISISVIGATQIKNTNKKYDFHSD--NSDKNGYKVRYPVSDYVNL 658
Db 593 NLANCQREKDISISVIGATQIKNTNKKIDFLSESNNEKNGYKVRYPVSDYVNL 652
Qy 659 SVKEEHGKCEAKCETVDSAEBSAQLKSSDTSERKRPDPSVYSTKDTKYQSVY 718
Db 653 SPKEERSKCEAKGSSNDSDESVNSVHSK--RDSERRRRPDSAYSTSKDTKYQSV 711
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QY 719 KQECIIATEV 728
Db 712 KQECIIATEV 721

RESULT 7
US-09-828-366-21
; Sequence 21, Application US/09828366
; Patent No. US2002010137A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klein, Robert D.
; APPLICANT: Napier, Mary
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P1694R1C1
; CURRENT APPLICATION NUMBER: US/09/828,366
; Prior filing data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 21
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-828-366-21

Query Match 84.1%; Score 3494.5; DB 9; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222; Indels 11; Gaps 7;
Matches 609; Conservative 47; Mismatches 64;

QY 1 MGRFLLTLLALLSALLCRQVDSGVFELKLOEFVNNKGLLSNRNCCRGGGGAGQOQC 60
Db 1 MGRCALALAVLSALL--CQVWSSGVFELKLOEFVNNKGLLGNRRCCR----GGAGPPPC 54

QY 61 DCKTFPRVCLKHQYQASVSPPEPCTYGSATITPVLGANSFVDPGAGADPAFNPPIRFPFG 120
Db 55 ACRTFPRVCLKHQYQASVSPPEPCTYGSATITPVLGVSFSLPDG--GGADSAFNPPIRFPFG 113

QY 121 FTWPGTFSLLIHALHTDSDPDLTTENPERLISRATQRLHVAEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFSLLIHALHTDSDPDLTTENPERLISRATQRLHVAEWSQDLHSSGRTDLKY 173

QY 181 SYRFVDEHYHGGSCVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db 174 SYRFVDEHYHGGSCVFCRPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233

QY 241 HGFCDKPGCKRVCWQGRYCDICIRYPCGLHGTCCQPMQCNQCBGWSGLFCNQDLNYCT 300
Db 234 HGFCDKPGCKRVCWQGRYCDICIRYPCGLHGTCCQPMQCNQCBGWSGLFCNQDLNYCT 293

QY 301 HHKPCNKGATCNTGQSYTCSRCPGYTGSCEIEINECDANPCKNKGSCDTLENSYCT 360
Db 294 HHKPCNKGATCNTGQSYTCSRCPGYTGSCEIEINECDANPCKNKGSCDTLENSYCT 353

QY 421 CANGAQCVDLGNSYICQCAQFTGRHCDNDVDDCASFPVNGGTCDGVNDVSYCTCPGY 480
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASFPVNGGTCDGVNDVSYCTCPGY 473

QY 481 NGKNCSTPVSRCHNPNCHNGATCHERSNYVCECARGYGLNCOELLPEPPGPGVVDFT 540
Db 474 TGRNCSAPVSRCHNPNCHNGATCHERSNYVCECARGYGLNCOELLPEPPGPGVVDFT 533

QY 541 EKYTEQNSQFPMIAYCAGIILVLLMLLGAALVVCRLVKQKRHHQBPACRSETETMNN 600
Db 541 EKYTEQNSQFPMIAYCAGIILVLLMLLGAALVVCRLVKQKRHHQBPACRSETETMNN 600

QY 534 EK-LEGQGPFPWAVACGAVILVLLMLLGAALVVCRLVKQKRHHQBPACRSETETMNN 592
QY 601 LANCOREKXDISISVIGATQIKNTNKKVDFHSDNS--DKNGYKYRYPVDYVNLVHKLKNE- 658
Db 593 LANCOREKXDISISVIGATQIKNTNKKADPHGHDHSDADKNGFKARYPAVDYVNLVQDLKGD- 652
QY 659 SVKEEHGKCEAKCETYDSEAEK-SAVOLKSDTTSERKRKPDVSVYSTSKDTKQSVVVIS- 717
Db 653 AVRDASHKRDYKCPQGSGBEKGTPPTLURGEASERKRKPDGSGCSTKDTKQSVVVIS- 712

QY 718 EKDECIATEV 728
Db 713 EKDECIATEV 723

RESULT 8
US-09-995-593A-9
; Sequence 9, Application US/09995593A
; Patent No. US20020128197A1
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP8447DIV
; CURRENT APPLICATION NUMBER: US/09/995,593A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 09/068,740
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-593A-9

Query Match 84.1%; Score 3494.5; DB 9; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222; Indels 11; Gaps 7;
Matches 609; Conservative 47; Mismatches 64;

QY 1 MGRFLLTLLALLSALLCRQVDSGVFELKLOEFVNNKGLLSNRNCCRGGGGAGQOQC 60
Db 1 MGRCALALAVLSALL--CQVWSSGVFELKLOEFVNNKGLLGNRRCCR----GGAGPPPC 54

QY 61 DCKTFPRVCLKHQYQASVSPPEPCTYGSATITPVLGANSFVDPGAGADPAFNPPIRFPFG 120
Db 55 ACRTFPRVCLKHQYQASVSPPEPCTYGSATITPVLGVSFSLPDG--GGADSAFNPPIRFPFG 113

QY 121 FTWPGTFSLLIHALHTDSDPDLTTENPERLISRATQRLHVAEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFSLLIHALHTDSDPDLTTENPERLISRATQRLHVAEWSQDLHSSGRTDLKY 173

QY 181 SYRFVDEHYHGGSCVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db 174 SYRFVDEHYHGGSCVFCRPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233

QY 241 HGFCDKPGCKRVCWQGRYCDICIRYPCGLHGTCCQPMQCNQCBGWSGLFCNQDLNYCT 300
Db 234 HGFCDKPGCKRVCWQGRYCDICIRYPCGLHGTCCQPMQCNQCBGWSGLFCNQDLNYCT 293

QY 301 HHKPCNKGATCNTGQSYTCSRCPGYTGSCEIEINECDANPCKNKGSCDTLENSYCT 360
Db 294 HHKPCNKGATCNTGQSYTCSRCPGYTGSCEIEINECDANPCKNKGSCDTLENSYCT 353

QY 421 CANGAQCVDLGNSYICQCAQFTGRHCDNDVDDCASFPVNGGTCDGVNDVSYCTCPGY 480
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASFPVNGGTCDGVNDVSYCTCPGY 473

QY 481 NGKNCSTPVSRCHNPNCHNGATCHERSNYVCECARGYGLNCOELLPEPPGPGVVDFT 540
Db 474 TGRNCSAPVSRCHNPNCHNGATCHERSNYVCECARGYGLNCOELLPEPPGPGVVDFT 533

QY 541 EKYTEQNSQFPMIAYCAGIILVLLMLLGAALVVCRLVKQKRHHQBPACRSETETMNN 600
Db 541 EKYTEQNSQFPMIAYCAGIILVLLMLLGAALVVCRLVKQKRHHQBPACRSETETMNN 600
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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-346

Query Match      84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy 1 MGRFLTLTALLSALLCRQVDSGVFELKQLQEFVNKKGLLSNNRCCRGPGGAGQOOC 60
Db 1 MGRFLTLTALLSALLCRQVDSGVFELKQLQEFVNKKGLLSNNRCCRGPGGAGQOOC 54
Qy 61 DCKTFRRVCLKHQYQASVSPPECTYGSATVPVLGANSFVDPGAGGADPAFNSNIRPPFG 120
Db 55 ACRTFFRRVCLKHQYQASVSPPECTYGSATVPVLGANSFVDPGAGGADPAFNSNIRPPFG 113
Qy 121 FTWPGTFLIIIEALHTDPSDDLTTENPERLISRLATQRLHLAGVBEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFLIIIEALHTDPSDDLTTENPERLISRLATQRLHLAGVBEWSQDLHSSGRTDLKY 173
Qy 181 SYRFVCDHEHYGEGSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db 174 SYRFVCDHEHYGEGSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233
Qy 241 HGFCDDKPECKRCRVGMQGRYCDCEIRYPCGLHGTCCQPPWQCNCOEGWGLFCNQDLNYCT 300
Db 234 HGFCDDKPECKRCRVGMQGRYCDCEIRYPCGLHGTCCQPPWQCNCOEGWGLFCNQDLNYCT 293
Qy 301 HHKPCKNKGCATCTNTGQSGYTCSCRPYGTGSSCEIENECDANPCNKGSCCTDLNSYSCT 360
Db 294 HHKPCKNKGCATCTNTGQSGYTCSCRPYGTGATCELGIDECDSPPCKNGSCCTDLNSYSCT 353
Qy 361 CPPGFYKNCBELSAMTCADGCFNGRCRDTNPDGGYSCRCPLGYSGFNCCKKIDYCS SSP 420
Db 354 CPPGFYKNCBELSAMTCADGCFNGRCRSDSPDGGYSCRCPCVGYSGFNCCKKIDYCS SSP 413
Qy 421 CANGAQCVDLGNYSYICOCQAGFTGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPGY 480
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPGY 473
Qy 481 NGKNCSTPVSRCBNPCHNGATCHERSNRYVCECARGYGGGLNCOFLLPEPPQGVIVDFT 540
Db 474 TGRNCSTPVSRCBNPCHNGATCHERSNRYVCECARGYGGGLNCOFLLPEPPQGVIVDFT 533
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAIIVVCRVLKVKQRHHQPEACRSETETMNN 600
Db 534 EK-LEGQGGPPWAVACAGVILVLMLLGCAIIVVCRVLKVKQRHHQPEACRSETETMNN 592
Qy 601 LANCOREKDISIVIGATQIKNTNKKYDHFSDNS-DKNGYKVRYPVDYNLVHLEKNE- 658
Db 593 LANCOREKDISIVIGATQIKNTNKKYDHFSDNS-DKNGYKVRYPVDYNLVHLEKNE- 652
Qy 659 SVKEHKGKCAKCTYDSEAEK-SAVQLKSSDTSERKRPSVSTSKDTKYQSVYVISE 717
Db 653 AVDAHAKRDTKCPQSSGEEKTPTTLRGEASERKRPSDGGCSTSKDTKYQSVYVISE 712
Qy 718 EKDECIATEV 728
Db 713 EKDECIATEV 723

RESULT 14
US-10-175-746-346
; Sequence 346, Application US/10175746
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; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C153
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-346

Query Match      84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy 1 MGRFLTLTALLSALLCRQVDSGVFELKQLQEFVNKKGLLSNNRCCRGPGGAGQOOC 60
Db 1 MGRFLTLTALLSALLCRQVDSGVFELKQLQEFVNKKGLLSNNRCCRGPGGAGQOOC 54
Qy 61 DCKTFRRVCLKHQYQASVSPPECTYGSATVPVLGANSFVDPGAGGADPAFNSNIRPPFG 120
Db 55 ACRTFFRRVCLKHQYQASVSPPECTYGSATVPVLGANSFVDPGAGGADPAFNSNIRPPFG 113
Qy 121 FTWPGTFLIIIEALHTDPSDDLTTENPERLISRLATQRLHLAGVBEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFLIIIEALHTDPSDDLTTENPERLISRLATQRLHLAGVBEWSQDLHSSGRTDLKY 173
Qy 181 SYRFVCDHEHYGEGSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db 174 SYRFVCDHEHYGEGSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233
Qy 241 HGFCDDKPECKRCRVGMQGRYCDCEIRYPCGLHGTCCQPPWQCNCOEGWGLFCNQDLNYCT 300
Db 234 HGFCDDKPECKRCRVGMQGRYCDCEIRYPCGLHGTCCQPPWQCNCOEGWGLFCNQDLNYCT 293
Qy 301 HHKPCKNKGCATCTNTGQSGYTCSCRPYGTGSSCEIENECDANPCNKGSCCTDLNSYSCT 360
Db 294 HHKPCKNKGCATCTNTGQSGYTCSCRPYGTGATCELGIDECDSPPCKNGSCCTDLNSYSCT 353
Qy 361 CPPGFYKNCBELSAMTCADGCFNGRCRDTNPDGGYSCRCPLGYSGFNCCKKIDYCS SSP 420
Db 354 CPPGFYKNCBELSAMTCADGCFNGRCRSDSPDGGYSCRCPCVGYSGFNCCKKIDYCS SSP 413
Qy 421 CANGAQCVDLGNYSYICOCQAGFTGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPGY 480
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASPPCVNGGTCCQGVNDYSCTCPGY 473
Qy 481 NGKNCSTPVSRCBNPCHNGATCHERSNRYVCECARGYGGGLNCOFLLPEPPQGVIVDFT 540
Db 474 TGRNCSTPVSRCBNPCHNGATCHERSNRYVCECARGYGGGLNCOFLLPEPPQGVIVDFT 533
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAIIVVCRVLKVKQRHHQPEACRSETETMNN 600
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Db 534 EK-LEGQGGPPFWAVCAGVILVLLGCAAVVVCVRLRLQKRRPPADPCRGETETMNN 592
QY 601 LANCOREKDISISVIGATQIKNTNKKVDPHSDNS-DKNGYKVRYPVDVNLVHELKNEB- 658
Db 593 LANCOREKDISISVIGATQIKNTNKKADPHGDSADKNGFKARYPAVDVNLVQDLKGGDT 652
QY 659 SVKEEHGKCEAKCETYDSEABEK-SAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717
Db 653 AVRDAHSKRDTKCQPGQSGSBEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISE 712
QY 718 EKDECIATEV 728
Db 713 EKDECVIATEV 723

RESULT 15
US-10-176-918-346
; Sequence 346, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-346

Query Match 84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALICRCQVDGSGVFELKIQEFVNNKGLLSNRNCCRGGGPGGAGQQQC 60
Db 1 MGRSCALAVLSALL--CQVWSSGVFELKIQEFVNNKGLLGNRNC--GGAGPPPC 54
QY 61 DCKTFRVCVKHYQASVSPPECTYGSALTIVLGANSFSVPDAGGADPAFNSNPIRFPFG 120
Db 55 ACRTFRVCVKHYQASVSPPECTYGSATPVLVGDSFSLPDG-GGADSAFNSNPIRFPFG 113
QY 121 FTWPGTFSLLIIBALHTDSPDDLTTENPERLISRLATQRLHAYGEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFSLLIIBALHTDSPDDLATENPERLISRLATQRLHAYGEWSQDLHSSGRTDLKY 173
QY 181 SYRFVCDHEHYGEGSVFCRPRDDRGHFTCCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240
Db 174 SYRFVCDHEHYGEGSVFCRPRDDAFGHFTCCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233
QY 241 HGFCDPKPGCKRCVQWQGRYCDDECIRYPGCLHGTCCQPMQCNQCBGSGGLFCNQDLNLYCT 300
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Db 234 HGFCDPKPGCKRCVQWQGRYCDDECIRYPGCLHGTCCQPMQCNQCBGSGGLFCNQDLNLYCT 293
QY 301 HHKPCKNKATCTNTQGGSYTCSRPGYTGSSCEIBINECDANPCKNKGGSCDTLENSYSCT 360
Db 294 HHKPCKNKATCTNTQGGSYTCSRPGYTGATGELGIDECDPSPCKNGGSCDTLENSYSCT 353
QY 361 CPPGYGKNCELSAMTADGPCFNGRCRTDNDPGYSCRCPLGYSGFNCEKIDYCSSSP 420
Db 364 CPPGYGKICEUSAMTADGPCFNGRCSDSPDGGYSCRCPVGYSGFNCEKIDYCSSSP 413
QY 421 CANGAQCVDLGNSYICQQAFTGRHCDNDVDDCAFFCVNGGTCCQDGYNDYSCTCPPGY 480
Db 414 CSNGAKCVDLGDAYLCRCQAGSGRHCDDNDVDDCASSPCANGGTCTRDGVNDFSCITCPPGY 473
QY 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGGLNCQFLPPEPPGPPVVDFT 540
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNQCQFLPPEPPGPAVDLT 533
QY 541 EKYTEGNSQPPWIAVCAGIILVLLGCAAVVVCVRLKVKQRHHQPEACRSETETMNN 600
Db 534 EK-LEGQGGPPFWAVCAGVILVLLGCAAVVVCVRLKQKRRPPADPCRGETETMNN 592
QY 601 LANCOREKDISISVIGATQIKNTNKKVDPHSDNS-DKNGYKVRYPVDVNLVHELKNEB- 658
Db 593 LANCOREKDISISVIGATQIKNTNKKADPHGDSADKNGFKARYPAVDVNLVQDLKGGDT 652
QY 659 SVKEEHGKCEAKCETYDSEABEK-SAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717
Db 653 AVRDAHSKRDTKCQPGQSGSBEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISE 712
QY 718 EKDECIATEV 728
Db 713 EKDECVIATEV 723

Search completed: November 29, 2004, 13:41:58
Job time : 77.3366 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2004, 13:16:29 ; Search time 18.2447 Seconds
(without alignments)
3839.238 Million cell updates/sec

Title: US-09-783-931-2
Perfect score: 4153
Sequence: 1 MGRFLTLALLSALLCRQ.....YQSVVISEKDECIATEV 728

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4153	100.0	728	2 I50719	C-Delta-1 - chicke
2	3407	82.0	722	2 I48324	DETA-like 1 - mou
3	1897	45.7	685	2 J07570	Delta-4 protein -
4	1863	44.9	686	2 J07569	Delta-4 protein -
5	1559.5	37.6	833	2 S19087	gene Delta protein
6	1555.5	37.5	832	2 A31246	neurogenic protein
7	1555.5	37.5	880	2 S00670	neurogenic repetit
8	1332.5	32.1	1220	2 A56136	jagged protein pre
9	1126.5	27.1	1408	2 S16148	gene serrate prote
10	815	19.6	2524	2 A35844	Kotch protein - Af
11	806.5	19.4	2437	2 S42612	transmembrane prot
12	793	19.1	2531	2 T31070	notch homolog - se
13	787.5	19.0	1064	2 A40136	fibropellin Ia - s
14	784.5	18.9	2703	1 A24420	notch protein - fr
15	781	18.8	1203	2 A49175	Notch B protein -
16	781	18.8	2531	2 A46019	notch-1 protein -
17	776.5	18.7	2471	2 A49128	cell-fate determin
18	776	18.7	2352	2 T30201	Notch homolog prot
19	775.5	18.7	2531	2 S18198	notch protein homo
20	754	18.2	2139	2 A35672	crumbs protein - f
21	754	18.2	2555	2 A40043	notch protein homo
22	749	18.0	2321	2 S45306	notch3 protein - h
23	732	17.6	2318	2 S45306	notch 3 protein -
24	709.5	17.1	1964	2 T09059	notch4 - mouse
25	694.5	16.7	570	2 A48836	fibropellin C prec
26	694.5	16.7	861	2 A48836	Notch homolog Motc
27	660	15.9	473	2 A56175	adhesive plaque pr
28	627	15.1	1372	2 T25933	hypothetical prote
29	626	15.1	385	2 S53718	homeotic protein d

protein FilC7.4 (i
preadipocyte facto
delta-like homeoti
glp1 protein precu
homeotic protein 1
slit-1 protein hom
secreted leucine-r
slit protein 2 pre
slit protein 1 pre
epidermal growth f
EGF repeat transme
hypothetical prote
protein F40E10.4 (i
MEGF5 protein - ra
Motch A protein -
intrinsic factor-B

ALIGNMENTS

RESULT 1
150719
C-Delta-1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50719
R:Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A:Title: Expression of a Delta homologue in prospective neurons in the chick.
A:Reference number: I50719; MUID:95319507; PMID:7596411
A:Accession: I50719
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <HEN>
A:Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:9882411; PID:988241
C:Superfamily: delta-4 protein; EGF homology
F:299-332/Domain: EGF homology <EGX1>
F:339-370/Domain: EGF homology <EGF1>
F:416-447/Domain: EGF homology <EGX2>
F:454-485/Domain: EGF homology <EGF>
F:492-523/Domain: EGF homology <EGF3>

Query Match 100.0%; Score 4153; DB 2; Length 728;
Best Local Similarity 100.0%; Pred. No. 3.3e-242;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGRFLTLALLSALLCRQVDGSGVPELKLQEFVNKKGLLSNRNCCRGCGGPGGAGQOQC 60
Db 1 MGRFLTLALLSALLCRQVDGSGVPELKLQEFVNKKGLLSNRNCCRGCGGPGGAGQOQC 60
Qy 61 DCKTFFRVCLKHVQASVSPBPCTYGSATPVLGANSFVDPGAGGADPAFSPNIRPPFG 120
Db 61 DCKTFFRVCLKHVQASVSPBPCTYGSATPVLGANSFVDPGAGGADPAFSPNIRPPFG 120
Qy 121 FTWPGTFLIIEALHTDSDPDLTTENPERLISRLATQRLHLAGVSEWSQDLHSSGRTDLKY 180
Db 121 FTWPGTFLIIEALHTDSDPDLTTENPERLISRLATQRLHLAGVSEWSQDLHSSGRTDLKY 180
Qy 181 SYRVCDEHYHGECSVFCPRDRDPGHFTCGERGEKVCNPGWKGVQYCTEPICLPGCDEQ 240
Db 181 SYRVCDEHYHGECSVFCPRDRDPGHFTCGERGEKVCNPGWKGVQYCTEPICLPGCDEQ 240
Qy 241 HGFCDKPECKRCVWGQGYCDECIRYPCGLHGTCCQPMWCNCOBGHGGGLFCNODLNYCT 300
Db 241 HGFCDKPECKRCVWGQGYCDECIRYPCGLHGTCCQPMWCNCOBGHGGGLFCNODLNYCT 300
Qy 301 HHKPKNGATCTNTGQGSYTCSCRPGYTGSSCEIENECDANPCKNCGSCTDLENSYSCT 360
Db 301 HHKPKNGATCTNTGQGSYTCSCRPGYTGSSCEIENECDANPCKNCGSCTDLENSYSCT 360
Qy 361 CPFGFYKNCNELSAMTCADGFCFNGRGCTNDPDGYSRCRPLGYSGFNGCKKIDYCSSSP 420

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Db 361 CPGPGFYKNCESLAMSACADGFCFNGGRCCTDNDPGGYSRCPLGYSGFNCEKKIDYCSSSP 420
QY 421 CANGAQCVDLGNSYICQCAQAGTGRHCHDDNDVDDCASFPVNGGTCDGVDNDYSCTCPGY 480
Db 421 CANGAQCVDLGNSYICQCAQAGTGRHCHDDNDVDDCASFPVNGGTCDGVDNDYSCTCPGY 480
QY 481 NGKNCSTPVSRCHEHNPCHNGATCHEBSNRYVCECARGYGGLNCOFLPEPPGPGPVVDFT 540
Db 481 NGKNCSTPVSRCHEHNPCHNGATCHEBSNRYVCECARGYGGLNCOFLPEPPGPGPVVDFT 540
QY 541 EKYTEGNSQFPWIAVCAGIILVLMLLGCAAIIVVCRVLKVQKRHHQPEACRSETETMNN 600
Db 541 EKYTEGNSQFPWIAVCAGIILVLMLLGCAAIIVVCRVLKVQKRHHQPEACRSETETMNN 600
QY 601 LANQOREKDISISVIGATQIKNTNKKVDPHSDNSDKNGYKVRYPVVDYNLHVKNEEDSV 660
Db 601 LANQOREKDISISVIGATQIKNTNKKVDPHSDNSDKNGYKVRYPVVDYNLHVKNEEDSV 660
QY 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVVISEKD 720
Db 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVVISEKD 720
QY 721 ECIATEV 728
Db 721 ECIATEV 728

RESULT 2
I48324
DELTA-like 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48324
R:Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
A:Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin
Development 121, 2407-2418, 1995
A:Reference number: I48324; MUID:95401858; PMID:7671806
A:Accession: I48324
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-722 <RES>
A:Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g806569; PIDN:CAA56865.1; PID:g8065
C:Genetics:
C:Gene: Dll1
C:Superfamily: delta-4 protein; EGF homology
F:331-362/Domain: EGF homology <EGF2>
F:446-477/Domain: EGF homology <EGF>
F:484-515/Domain: EGF homology <EGF1>

Query Match 82.0%; Score 3407; DB 2; Length 722;
Best Local Similarity 79.5%; Pred. No. 2.2e-197;
Matches 581; Conservative 71; Mismatches 67; Indels 12; Gaps 6;

QY 1 MGRFLLTLALISALLCRCQVDGSGVFELKLOEFVNNKGLLSNRNCRGG-GPGGAGQQQ 59
Db 1 MGRSALALAVSALL--CQVSSGVFELKLOEFVNNKGLLSNRNCRGGSGP-----P 52
QY 60 CDCKTFRRVCLKHQYASVSEPPCTVGSAITPVLGANSFSPDGAGADPAFSPNIRFPF 119
Db 53 CACRTFFRVLKHQYASVSEPPCTVGSAVTPVLGDSFSLPDGA-GIDPAFSPNIRFPF 111
QY 120 GFTWPGTFFSLIILALHTDSPDLLTTENPERLLSRLATORHLAVGEWSQDLHSSGRTDLK 179
Db 112 GFTWPGTFFSLIILALHTDSPDLLATENPERLLSRLTTQRHLTVGEWSQDLHSSGRTDLR 171
QY 180 YSYRVCDDHYHGECSVFCRDRDRFGHFTCGERGEKVCNPGWKQYCTEPICLPGCDE 239
Db 172 YSYRVCDDHYHGECSVFCRDRDDAFGHFTCGERGEKVCDFGWKQYCTDPICLPGCDD 231
QY 240 QHGFCDKPGCKRCVWGQGRYCDICIRYPCGLHGTCCQPWQNCQEGWGLFCNQDLNYC 299
Db 232 QHGFCDKPGCKRCVWGQGRYCDICIRYPCGLHGTCCQPWQNCQEGWGLFCNQDLNYC 291
```

```
QY 300 THHKPKNGATCTNTGQSYTCSCRPGYTGSSCEITEINECDANPCKNGSSCTDLENSYC 359
Db 292 THHKPCRNGATCTNTGQSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSC 351
QY 360 TCPPGFYKNCESLAMSACADGFCFNGGRCCTDNDPGGYSRCPLGYSGFNCEKKIDYCSSS 419
Db 352 TCPPGFYKNCESLAMSACADGFCFNGGRCSDNDPGGYTCHCPLGFSGFNCEKKMDLCSGS 411
QY 420 PCANGAQCVDLGNSYICQCAQAGTGRHCHDDNDVDDCASFPVNGGTCDGVDNDYSCTCPG 479
Db 412 PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDVDDCASSPCANGGTCDSDVNDFSCTCPG 471
QY 480 YNGKNCSTPVSRCHEHNPCHNGATCHEBSNRYVCECARGYGGLNCOFLPEPPGPGPVVD 539
Db 472 YTGKNCSPVSRCEHAPCHNGATCHQGRQRYNCECAQGGGNCQFLPEPPPGPMVVDL 531
QY 540 TEKYTEGNSQFPWIAVCAGIILVLMLLGCAAIIVVCRVLKVQKRHHQPEACRSETETMNN 599
Db 532 SERHMSQGGPPWAVACAGVVLVLLLLGCAAVVCRVLKLQKHQPPPEPCGGETETMNN 591
QY 600 NLANCQREKDISISVIGATQIKNTNKKVDPHSDN--SDKNGYKVRYPVVDYNLHVK-NE 657
Db 592 NLANCQREKDVSVSIIGATQIKNTNKKADPHGDHGAKKSSFKVRYPTVDYNLVRDLKGD 651
QY 658 DSVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVVIS 717
Db 652 ATVRDTHSKRDKCOSQSAGEEKIAPTIRGGEIPDRKRPSVYSTSKDTKYQSVVLSA 711
QY 718 EKDECIATEV 728
Db 712 EKDECVIATEV 722

RESULT 3
JC7570
Delta-4 protein - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7570
R:Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A:Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A:Reference number: JC7569; MUID: 21064937; PMID:11134954
A:Accession: JC7570
A:Molecule type: mRNA
A:Residues: 1-685 <YON>
A:Cross-references: UNIPROT:Q9NR61; DBJ:AB043894
C:Comment: This protein, a member of the Notch family of proteins, is a transmembrane rec
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C:Genetics:
A:Gene: delta-4
C:Superfamily: delta-4 protein; EGF homology
C:Keywords: transmembrane protein

Query Match 45.7%; Score 1897; DB 2; Length 685;
Best Local Similarity 48.2%; Pred. No. 1.1e-106;
Matches 552; Conservative 112; Mismatches 195; Indels 72; Gaps 18;

QY 11 LLSALLCRCQVDGSGVFELKLOEFVNNKGLLSNRNCRGGGPGGAGQQQCDCKTFRVCL 70
Db 14 LLLVALWQRAAGSGVFQLQLEFINERGLASGRPCPG-----CRTFRVCL 62
QY 71 KHYQASVSEPPCTVGSAITPVLGANSFSPDGACGADPAFSPNIRFPFGTPWPGTFFSLI 130
Db 63 KHFAQVAVSP-GPCTFTVSTPVLGTSFAVRDSSGGG---RNPLQLPFNFWPGTFFSLI 118
QY 131 TEALHTDSPDLLTTE--NPERLLSRLATORHLAVGEWSQDLHSSGRTDLKYSYRFVCD 188
Db 119 IEAWHAPG-DDLRPALPDPALISKIALQGSILAVQNLWLLDEQSTLTFLRLSYRIVCSD 177
QY 189 HYYGEGCSVFCRDRDRFGHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQHGCDKPG 248
Db 178 NYYGDNCSRLCKRNDHFGHYVVCQPDGNLSCLPGWTGVCQQPICLSGCHEQNGVCSKPA 237
```


Qy	187	DEHYEGGCVFCRPRDRRDEGHFTGCTGSRGKVCNPGWKGYCTBPICLPGCDEQHGFCDK	248
Db	177	SDNYGESCRLCKKRRDHFHGYECQPDGSLSCLPGWTKYCDQPCILSGCHEQNGYCSK	236
Qy	247	PGECKRCHVQGRYCDBCIIRYPGCLHGTCTOOPQOCNCQBGWGLFCNQDLNCTYTHHPCK	306
Db	237	PDECICRPGWQGRCLNCEICPHNGCRHGTCTIPMQACDEGWGLFCQDQDLNCTYTHHSPCK	296
Qy	307	NGATCTNTGQSYTCSRCRPGYTGSSCEIENECNANPKNGSGCTDLENSYSCTCPGPGY	366
Db	297	NGTCSNSGPGYTGCTCLPGTTEHCELGSLKCSNPNCRNGSGSKDQENSYHCLCLPPGYY	356
Qy	367	GKNCELSAMTCADGCPFNNGRCTD-NPDGGYSRCPLGYSGFNCEKKIDYCSSSPCANGA	425
Db	357	GOHCEHSTLTCA DSPCFNGGSCRRNQGSSYACBPNETGSCNCKKVDRCSTSNPCANGG	416
Qy	426	QCVDLGNYSYICQOAGATGHRHCDNDVDDCASFPVCVNGGTCTODGVNDYSCCTCPGYNGKVC	485
Db	417	QCQNRGSPSRTCRRPGTGTGTHCLHISDCARSPCAHGSGTCHDLENGVCVCTCPAGSGRR	476
Qy	486	STPVSR--CEHNPNCHNGATCHE--RSNRVYCECARGYGLNCGCTLLPEPPQGPVIVDFTE	541
Db	477	EVRTIHDAKASGCFNGATCTYGLSPNPNVCNCPYGFVGRCEPVGLP--	526
Qy	542	KYTEGONSQPPYIAVCAGIITLVMLLLGCAAIYVVCVRLKVQKRHHQPEACRSETETMNNL	601
Db	527	-----SPFWAVSIVGLVLLVL-LVMVVAVR--QLRLRRPD--DESREAMNNL	572
Qy	602	ANCOREKDISIVIGATQIKNTNKKVDVFDHSD-NSDK-NGYKRVPSVDYNLVHLEKHNEDS	659
Db	573	SDPQD-----NLIPAAQLKNTNKKQKLELYDVCGLDKSNCGKLNHTLDYNLAPGLLG---	624
Qy	660	VKEHGKCEAKCTYSEBAEKSAVOLKSSDTSERKPD---SVYSTSKTKTKQSVVVIS	716
Db	625	-----RGMPGPKYPHSDKSLGEKVPRLHS-----EKPECRI SAICSPRDSMYOSVCLIS	674
Qy	717	ERKDECIITAEV 728	
Db	675	EERNECVIAEV 686	
RESULT 5			
S19087			
gene Delta protein precursor - fruit fly (Drosophila melanogaster)			
C:Species: Drosophila melanogaster			
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004			
C:Accession: S19087			
R;Muskavitch, M.A.T.			
submitted to the EMBL Data Library, June 1991			
A:Reference number: S19087			
A:Accession: S19087			
A>Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-833 <MUS>			
A:Cross-references: UNIPROT:P10041; EMBL:Y00222			
C:Genetics:			
A:Gene: FlyBase:D1			
A:Cross-references: FlyBase:FBgn0000463			
C:Superfamily: neurogenic protein delta; EGF homology			
F:335-371/Domain: EGF homology <EGF1>			
F:378-415/Domain: EGF homology <EGX1>			
F:457-488/Domain: EGF homology <EGF>			
F:533-564/Domain: EGF homology <EGF3>			
Query Match 37.6%; Score 1559.5; DB 2; Length 833;			
Best Local Similarity 42.4%; Pred. No. 2.4e-86;			
Matches 292; Conservative 83; Mismatches 241; Indels 73; Gaps 14;			
Qy	11	LLSALLC---RCQVDGSGVFELKQLQEFVNKKLLSNRNCRCGGPGGAGQQQCCDCKTFFR	67
Db	7	LITAFCTFVIVGVHSSGSEFELKLYFSDHGDNRDNEGRCCSGSDGATGKLGCSCKTFR	66

A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;457-488/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>

```
Query Match          37.5%; Score 1555.5; DB 2; Length 880;
Best Local Similarity 42.2%; Pred. No. 4.4e-86;
Matches 291; Conservative 85; Mismatches 240; Indels 73; Gaps 14;

Qy 11 LLSALLC---RCQVDGSGVFELKLOEFVNKGLLSNRNCCRGGGGGAGQOQOCDKTFPR 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7  LLLAFICPTVIVQVHSSGSFELRLKYFSDNHRDNEGRCCSGESDGTGKGLGSKCTKTR 66

Qy 68 VCLKHQYQASVPEPCTYGSALTIVLGANSVSPDAGGADAPASNPIRPFPGTWPTTF 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 LCLKHQYQATIDTTSQCTYGDVITPILGENSVNLDAQRFQNGFTNPIDPFPSWPGTF 126

Qy 128 SLIIIEALHTDSPDOLLTTENPERLISRATQRLHVAEGEWSQDLHSSGRTDLKYSYRFVCD 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 SLIIVEAWH-DTNNNSNARTNKLQRLVQVLEVSSEWKTNKSESQYTSLEYDFRVTC 185

Qy 188 EHYEGEGSVFCPRDRDRFGHFTCBERGEKVCNPGWKQGYCTEPICLPGCDEQHGFCDKP 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 186 LNYTSGSCAKFCPRDRDSFGHSTCSETGEIILCTGWQDGYCHIPKCAKGC--EHGHCDKP 243

Qy 248 GECKRVGWQGRYDCECIRYPGCLHGTCCQPMQNCQEGWGLFCNQDLNYCTHHKCKEN 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 NQCVQLGWKALCNECVLEPNCIHGTCKNFWPTICNEGWGLYCNQDLNYCTNHRPCKN 303

Qy 308 GATCNTNGQSYTCSCRPGYTGSGEIEINECDA--NPCKNGGSGCTD---LENSYSTCPC 362
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 GGTCTNTGEGLYTCKCAPGYSDDCENEIYSCDADVPQNGGTCIDEPHTKTYKCHCR 363

Qy 363 PGFYGNKCELSAMTADGCPNPGRCRTNPDG-----GYSCRPLGYSGFNCBKKIDYC 416
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 NGWSGKMCCEKVLATCSDKPC-HQGITCRNVRPLGSKGQGYCECPYIGVSGNCDLQDLNC 422

Qy 417 SSSPCANGAQ-----CVDLGNSTYCCQAG 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 423 SPNFCINGGSCQPSGKICIPSGFSGTRCETNIDCLGHQCENGGTCIDMNVQYRCQCPVG 482

Qy 442 FTGRHCDNDVDCAFPVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGA 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 FHGTHCSKVDCLIRPCANGGTCNLNNDYQCTCRAGFTGKDCSVIDECSSGFCNNG 542

Qy 502 TCHERSNRYVCECARGYGLNCOFLPPEPPQGPVVD-----FTEKYTEG-QNSQFPWI 554
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 543 TCMNRVNSFEVCVANGFRGKQCD---EESYDSVTFDAHQYGATTQARADGLANAQVVL 598

Qy 555 AVCAGIILVLLGLGCAIIVCVRLKVQKRHHQPEACRSETETWNLANCOREKDIDISV 614
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 599 AVFSVAMPLVAVIAAC--VWFCMKRK-RKRAQEKDABARKQNEQNAVATMHNGSAVG 655

Qy 615 -----IGATQIKNTNKKVDPHSDNSDKN 637
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 ALASASMGKGTGSGNSGLTFDGGNPNIIKN 684
```

RESULT 8
A56136
jagged protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
C;Accession: A56136
R;Lindesell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
Cell 80, 909-917, 1995
A;Title: Jagged: a mammalian ligand that activates Notch1.
A;Reference number: A56136; MUID:95211842; PMID:7697721
A;Accession: A56136
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-1220 <LIN>
A;Cross-references: GB:L38483
F;379-410/Domain: EGF homology <EGF1>
F;492-523/Domain: EGF homology <EGF>
F;634-665/Domain: EGF homology <EGF2>

```
Query Match          32.1%; Score 1332.5; DB 2; Length 1220;
Best Local Similarity 41.9%; Pred. No. 1.5e-72;
Matches 236; Conservative 77; Mismatches 193; Indels 57; Gaps 10;

Qy 9  LALLSALLC---RCQVDG--SGVFELKLOEFVNKGLLSNRNCCRGGG-----PGGAGQOQCD 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 14 LSLALLCALRAKAVCGASQGFELILSMQNVNGELQNGNCACBPGTLVRPYKCTDRBCD 73

Qy 62 CKTFERYCLKHQYQASVPEPCTYGSALTIVLGANSVSPDAGGADAPASNPIRPFPGF 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 --TYFKVCLKEYQSRVTAGGCSFGSGSTPVIGGTFNLIKASRGND-----RNRIVLPSPF 127

Qy 122 TWPQTFSLIIIEALHTDSPDOLLTTENPERLISRATQRLHVAEGEWSQDLHSSGRTDLKYS 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 AWPRSYTLLEA--WDSND--TIQPDIIIEKASHSGMINFSPQWQTLKQNTGIAHPEYQ 183

Qy 182 YRFVCDHYEGEGSVFCPRDRDRFGHFTCBERGEKVCNPGWKQGYCTEPICLPGCDEQ 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 IRVTCDDHYGFGCNKFCPRDRDFGHYACDQNGNKTMEGWMGPECNKAICROGCSPKH 243

Qy 242 GFCDKPGCEKRVGWQGRYDCECIRYPGCLHGTCCQPMQNCQEGWGLFCNQDLNYCTH 301
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 GSCKLPDGCRCQGWQGLYCDKCLPHPGCVHGTCTNEPQWCLCETNMGWGLCDKDLNYCGT 303

Qy 302 HKPCNKAGATCNTNGQSYTCSCRPGYTGSGCEI----- 334
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 HQPLNRTGTSNTGPDYKQCSCEPGYSGPNCEIAEACLSDPCHNRSGCKTSSGFCEC 363

Qy 335 -----EINECDANPCXNGGSCSTDLENSYSTCPCPGFYGNKCELSAMTADGCPFC 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 SPGWGTGTCSTNIDDCSPNNCSHGTCQDLVNGFKVCVPPQWTKTQOLDANECEAKPCV 423

Qy 384 NGRCRTNPDGGYSCRCPLGYSGFNCBKKIDYCSSSPCANGAOCVDLGNSTYCCQAGFT 443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 NARSC-KNLIASYCDDLPGMGMQNCNDINCLGQ--CONDASCRDLVNGYRCICPPGYA 481

Qy 444 GRHCDNDVDCAFPVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGATC 503
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 GDHCERIDDECAENPCLNGCHQCNEINRFQCLCTGFSGNLCQLDIDYCEPNPQNGAQ 541

Qy 504 HERSNRYVCECARGYGLNCOFL 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 YNRASDYFCKPCPEDEYEGKNGSHL 564
```

RESULT 9
S16148
gene serrate protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16148; S16878; A36666
R;Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a co-
A;Reference number: S16148; MUID:91347903; PMID:1840519
A;Accession: S16148
A;Molecule type: mRNA
A;Residues: 1-1408 <THO1>
A;Cross-references: UNIPROT:P18168; EMBL:X56811
R;Thomas, U.
submitted to the EMBL Data Library, November 1990
A;Reference number: S16878
A;Accession: S16878
A;Molecule type: mRNA
A;Residues: 1-1351, 'T', 1353-1408 <THO2>
A;Cross-references: EMBL:X56811; NID:g8563; PID:g8564

Db 810 VAGYKNCMLPYTGAIACBAVLAPCAGSPCKNGGRCKESEDFFETSCBPPHQQGOTCID 869

Qy 296 LNYCTHHKPCNKNGATCTTNGQSYTCSCRPYGTGSSCSBIEINECDANPCXNGGCTDLEN 355

Db 870 MNECV-NRPRNGATCQNT-NGSYKCNCKPGYTGRCENEMDIDDCQPNCHNGGSCSDGIN 927

Qy 356 SYSTCTCPGPGYKNCSELSAMTACADPCFNGRCRTNPDGGYSCRCPLGSGFNCBKKIDY 415

Db 928 MFFCNCPAGFRPKCEEDINECASPNCKNGANCCTDCVN-SYTCTCQPGFSGIHCBESNTPD 986

Qy 416 CSSSPCANGAOCVDLGNYSYICQOAGFTGRHCDNDVDCASFPCCVNGGTCCDGVNDYSCT 475

Db 987 CTESCFNGGTICIDINTFTQCPEFTGSGYQHIDNECDKSPCLNGGTCCDSYGTAKT 1046

Qy 476 CPPGYNGKNCSTPVSRCHNPNCHNGATCHEHSNRYVCECARGYGGLNC 523

Db 1047 CPQGYTGLNCQLVRWCDSPPCKNGKCKWQTNFYRCCKSGWTGVYC 1094

RESULT 11

S42612

transmembrane protein precursor - zebra fish

C:Species: Brachydanio rerio (zebra fish)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S42612

R:Bierkamp, C.; Campos-Ortega, J.A.

Mech. Dev. 43, 87-100, 1993

A:Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern

A:Reference number: S42612; MUID:94128602; PMID:8297791

A:Accession: S42612

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2437 <BIE>

A:Cross-references: UNIPROT:P46530; EMBL:X69088; NID:9433866; PIDN:CAA40831.1; PID:94338

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

F:755-786/Domain: EGF homology <EGF>

F:1023-1054/Domain: EGF homology <EGF>

F:1185-1216/Domain: EGF homology <EGF2>

F:1915-1947/Domain: ankyrin repeat homology <AN1>

F:1948-1980/Domain: ankyrin repeat homology <AN2>

F:1982-2014/Domain: ankyrin repeat homology <AN3>

F:2015-2047/Domain: ankyrin repeat homology <AN4>

F:2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 19.4%; Score 806.5; DB 2; Length 2437;

Best Local Similarity 27.3%; Pred. No. 1.1e-40;

Matches 190; Conservative 69; Mismatches 195; Indels 241; Gaps 26;

Qy 12 LSALLCRQVDGSG-VPELKLQEFVFNKKGLLSNRNCRGGG-----PGGAGQ 57

Db 582 VASFTCDRCPGYTGRLCETNINECLSQP-----CRNGGTCCDRENAVICTCPKGTG 633

Qy 58 QQC-----DCKTFRVCLKHQASVSPEPPCTYGSATIPVLGANSFVDPDAG-----GA 107

Db 634 VNCBINDDCK-----RKPCDYKCKIDKINGEYCEVCEPGYSGMNCINI 677

Qy 108 DPAFSNPIRPFPGFTWPGTFLIIEALHTDSPDLTTENPERLISRLATORHLAVGEWS 167

Db 678 DDCAINPCN-----GGTC-----IDGVNFTCLCPDPRDATCLSOH-----NECS 719

Qy 168 QD--LHSSGRITDKYSYRPFVCDHYEGGCSV-----FCRPRDRFRGFTC 211

Db 720 SNPCIHSGSLDQIN-SYRCVCEAGMGRNCDININECLSNPCVNGGTCK---DMTSGYLC 775

Qy 212 GERGEKVCNPGWKQYCTEPI-----CL--PGC-DEQHGFCDPKPECKRCVWQGRYC 261

Db 776 -----TCRAGFGSPNCOMINECASPNCLNQSGCIDDVAGF-----KCNMLPYTGEVC 824

Qy 262 DE-----CIRYPGCLHGTQ-----QPMQCNQEGWGLFCNODLNYCTHHKPCNKNGATCT 312

Db 825 ENVLAPCSPRCKNGGVCRESEDFQSFSCNCPAGWQGTCEVDINECVRN-PCNTNGVCE 883

Qy 313 NTGQGSYTCSCRPGYTGSSCSBIEINECDAN----- 342

Db 884 NL-RGGFCQRCNPGFTGALCENDIDDCBPNPCSNGVQCQDRVNGFVCLAGFRGERCAE 942

Qy 343 -----PCKNGGSCDTLENSYCTCPPPGYKNCSELSAMTACADPCFNGGRCTDN--- 391

Db 943 DIDEVSAAPCRNGNCTDCVNSYTCSPAGFSGINCEINTPDCTESSCFNGGTCTVDGLSS 1002

Qy 392 -----PDGG-----YSCRCPLGYSGFNCEKIDYCS 417

Db 1003 FSCVCLPGFTGNYCQHDVNECDSPCQNGGSCQDGYGYKCTCPHGYTGLNCQSLVRWCD 1062

Qy 418 SSPCANG-----AQVCD 429

Db 1063 SSPCKNGGSCWQOGASFTCCASGWTGIYCDVPSVCEVAARQOQSVAVLCRHAGOCVD 1122

Qy 430 LGNSYICQOAGFTGRHCDNDVDCASFPCCVNGGTCCDGVNDYSCTCPPGYKNCSTPV 489

Db 1123 AGNTHLCRCQAGYTGSCQEQVDECQNPQNGATCTDYLGYSCECVPGYHGMNCKEI 1182

Qy 490 SRCEHNPCHNGATCHEHSNRYVCECARGYGGLNCQ 524

Db 1183 NECLSQPCQNGGTICDLVNTYKCSCPRGTOGVHCE 1217

RESULT 12

T31070

notch homolog - sea urchin (Lytechinus variegatus)

C:Species: Lytechinus variegatus (variegated urchin)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000

C:Accession: T31070

R:Sherwood, D.R.; McClay, D.R.

Development 124, 3363-3374, 1997

A:Title: Identification and localization of a sea urchin Notch homologue: insights into

A:Reference number: Z20966; MUID:97454256; PMID:9310331

A:Accession: T31070

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2531 <SHE>

A:Cross-references: EMBL:AF000634; NID:92570350; PID:92570351; PIDN:AAB82088.1

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 19.1%; Score 793; DB 2; Length 2531;

Best Local Similarity 30.6%; Pred. No. 7.3e-40;

Matches 184; Conservative 80; Mismatches 231; Indels 106; Gaps 23;

Qy 2 GGRFLTLALLSALLCRQV-----DGSQVPELK-----LQEFVFNKKGLLSNRN 45

Db 495 GGVACICLTGTGLCTETDINECSSNPCLNGASCDFITGRFEACLAGYTTTCQVNIID 554

Qy 46 C---CRGGGP--GGAGQQCDCKTFRVCLKHQASVSPEPPCTYGSATIPVLGANSFS 99

Db 555 CQSSPCENGTCIDGVNQFTCLCETGYEGHRCMDSDCASRPCMNGGVCEDLIGFYQCN 614

Qy 100 VPDGAGADPAF-----SNPIRPFPGFTWPGTFLIIEALHTDSPDLTTENPERLIS 153

Db 615 CPVGTSGDNCEYNHYDCSSNP-----CVNDGTCVDGNEYTCMCHE----- 655

Qy 154 LATQRHLAVGEE-----WSQDLHSSGR-TDLKYSYRPFVCDHYEGGCSVCECRPR----- 202

Db 656 --GYRGLNCEBIDDCESRPCNHNGGTCTDVBWNGHYCLCPGYH-----DPPCMNSINECSS 709

Qy 203 -----DDRFGHTCGERGEKVCNPGWKQYCTEPI-----CLPG--CDEQHGFC 244

Db 710 NPCVNGSGCHDGVNEYSV-----ECMAGYTGRTCTDDFDECSNPNCHGGTCDNRHAFY 763

Qy 245 DKPGECKRCRVGWQGRYC-----DECIRYPGCLH-GTC---QPMQCNQEGWGLFCNODL 296

Db 764 N-----CTCOAGYTGLENCEVNIDDCVDEP-CLNGGICIDEVNSFCVCPQTFFVGLLCETER 818

Qy 297 NYCTHHKPCNKNGATCT-NTGQGSYTCSCRPGYTGSSCSBIEINECDANPCXNGGCTDLEN 355

Db 819 SPCEDNQ-CQNGATCVYSYEDYAGYSCRCTSGFGNFCDDDRNCLFSPCRNGSGSCTNLEG 877

notch protein - fruit fly (*Drosophila melanogaster*)
N:Alternate names: neurogenic repetitive locus protein
C:Species: *Drosophila melanogaster*
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: A24420; A24768; S09358; A05267
R:Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A:Reference number: A24420; MUID:87064624; PMID:3097517
A:Accession: A24420
A:Molecule type: DNA
A:Residues: 1-2703 <KID>
A:Cross-references: UNIPROT:P07207; GB:K03508; NID:gl57991; PIDN:AAA28725.1; PID:gl57993
R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A:Reference number: A24768; MUID:86079539; PMID:3933325
A:Accession: A24768
A:Molecule type: mRNA
A:Residues: 1-48, 1'-50-118, 'R', 120-230, 1', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, 'R'; Tautz, D.
Nucleic Acids Res. 17, 6463-6471, 1989
A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA markers
A:Reference number: S09358; MUID:89385974; PMID:2780284
A:Accession: S09358
A:Molecule type: DNA
A:Residues: 2505-2551, 'OQQQ', 2552-2576, 'E', 2578-2604 <TAU>
R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A:Title: Opa: a novel family of transcribed repeats shared by the Notch locus and other
A:Reference number: A05267; MUID:85099329; PMID:2981631
A:Accession: A05267
A:Molecule type: DNA
A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>
C:Genetics:
A:Gene: notch; opa
A:Cross-references: FlyBase:FBgn0004647
A:Map position: 8.96-9.36
A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C:Keywords: differentiation; tandem repeat; transmembrane protein
F:27-43/Domain: transmembrane #status predicted <TMW1>
F:297-328/Domain: EGF homology <EGX1>
F:530-561/Domain: EGF homology <EGF1>
F:568-599/Domain: EGF homology <EGF>
F:988-1019/Domain: EGF homology <EGX2>
F:1064-1095/Domain: EGF homology <EGF3>
F:1187-1218/Domain: EGF homology <EGX3>
F:1746-1762/Domain: transmembrane #status predicted <TMW2>
F:1950-1982/Domain: ankyrin repeat homology <AN1>
F:1983-2015/Domain: ankyrin repeat homology <AN2>
F:1988-2004/Domain: transmembrane #status predicted <TMW3>
F:2017-2049/Domain: ankyrin repeat homology <AN3>
F:2050-2082/Domain: ankyrin repeat homology <AN4>
F:2083-2115/Domain: ankyrin repeat homology <AN5>
F:2538-2568/Region: glutamine-rich
F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 18.9%; Score 784.5; DB 1; Length 2703;
Best Local Similarity 35.2%; Pred. No. 2.5e-39;
Matches 151; Conservative 52; Mismatches 139; Indels 87; Gaps 10;

Qy 167 SLDLHSSGRTDLKYSYRFVCDHEHYGEGCS-----VFCKPRDDREGHFTCGERG 215
Db 608 SNPCHRGKCIDVNSFKCLDPGYTYGICQKQINECSNPFQFGHCODRVGSYYC----- 663

Qy 216 EKVNPNGKGYCTEPI-----CLPGCDEQHGFCDXGBCCKRVGQGRYC- 261
Db 664 --QCQAGTSGKNCVNVNNECHSNPNNGATCIDGINSY-----KCQCVPFGTGQHC 713

Qy 262 ---DECIRYPCCLHGTC---OQPQNCNCEQEWGLFCNQDLNYCTHHKPCNKGATCNTG 315
Db 714 KNVDECISPPCANNGVCIDQVNGYKCEPRFGYDAHCLSDVDECASN-PCVNEGRCED-G 771

Qy 316 QGSYTCSRPGYTGSSCEIEINECDAMPKNGSGSTDLNLSYSCTCPGFGYGNKNCELSAM 375
Db 772 INEFICHCPGYTKRCELDIDECSSNPCQHGCTCYDKLNAFSCQCMGTYGQKCEINID 831
Qy 376 TCADGPFNGRCRTNPDG-----GQY 396
Db 832 DCVTNPGNGGTCIDKVNKYCKVCPFTGRDCESKMDPCASNRCTKNAKCTPPSSNFLDF 891
Qy 397 SCRCPLGVSGFNCSEKKIDYCS-SSPCANGAOCVDLGNLSYICQCGAGFTGRHCDNDVDDCA 455
Db 892 SCTLKLGTYGRYCUDEDIDECSLSPCRNGASCLNVPGSYRCLCTKGYEGRDCAINTDDCA 951
Qy 456 SFPVNGGTCODGVNDYSCTCPGNGKNCSTPVSRCBNPCHNGATCHEHSRNYVCECA 515
Db 952 SFPQNGGTCLDIGDYSLCVDGFDGKHCBTDINECLSQPCQNGATCSQVNSYVCTCTCP 1011
Qy 516 RGYGLNCQ 524
Db 1012 LGFSGINCO 1020

RESULT 15
A49175
Notch B protein - mouse (fragment)
N:Alternate names: Notch homolog
C:Species: *Mus musculus* (house mouse)
C>Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change 16-Aug-2004
C:Accession: A49175; PH1570; S32113
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <LAR>
A:Cross-references: UNIPROT:O35516; EMBL:X68279; NID:G287989; PIDN:CAA48340.1; PID:G2879
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision between
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:143-174/Domain: EGF homology <EGX1>
F:492-513/Domain: EGF homology <EGF1>
F:560-591/Domain: EGF homology <EGF>
F:674-705/Domain: EGF homology <EGX2>
F:712-743/Domain: EGF homology <EGF3>
F:836-867/Domain: EGF homology <EGX3>

Query Match 18.8%; Score 781; DB 2; Length 1203;
Best Local Similarity 29.5%; Pred. No. 2e-39;
Matches 189; Conservative 69; Mismatches 194; Indels 188; Gaps 26;

Qy 45 NCRGGGPGGAGQQQCDCKTFFRVCLKHQASVPEPPCTYGSAITPVLGANSFSPDGA 104
Db 315 NC-----QPGTSG---LNCEINFDDCASN-----PCMHGVCDV---GINRYSCVCSP 355

Qy 105 G-----CADPAPSNPIR-----PPFGFTWPGTFSLIILALHTDSDPD 141
Db 356 GPTGQRNCNIDIDECASNPCRCRGATCINDVNGFRICPEGPHHPSCYQVNECL----- 408

Qy 142 LTTENP---BRLISRLATORHLA---VGEWESODLH-----SSGRT--DLKYSYRFV 185
Db 409 ---SNPCIHNCCTGGISGYKCLCDAGHWGVNCEVDKNECLSNPCQNGGTCNNLVNGYRCT 465

Qy 186 CDBHYHGECSV---FCRPR-----DDRFHFTCGERGEKVCNPNMGQYCTEPI- 232
Db 466 CKXGFXGYNQVNIDECASNPCNLNQGTCFDDVSG-YTCH-----CMLPYTGKNCQVLA 518

Qy 233 -CLPGCDEQHGFC-DKPG-----ECKRVGQGRYC-----DECIRYPCCLHGTC---OQPW 279
Db 519 PCSPNFCENAAVKEAPNPFESFSCLPAGWQGRKRTVDVDECISKPCMNNGVCHNTQGSY 578

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QY 280 QCNQCBGGLFCNODLNYCTHHKPCXNGATCTNTGGSYTCSCRPGYTGSSCEIEINEC 339
Db 579 VCECPFGSGMDCEEINDCLAN-PCQNGSCVD-HVNTFSCQCHPGFIGDKCQTDMMNEC 636
QY 340 DANPCXNGGCTDLENSYSCTCPPPGYGNKCELSAMTCADGPCFNGGRCTD----- 390
Db 637 LSEPCXNGGCTSDYVNSYCTCPAGPHGVHCENNIDECTESSCFNGGTCVDGINSFSLC 696
QY 391 -----NPD-----GGYSCRPGLYSGFNCEKKIDYCSSSPCA 422
Db 697 PVGFTGPFCLHDINECSSNPLNAGTCVDGLGTYRCICPLGYTGKNCQTLVNLCSRSPCK 756
QY 423 N-----GAQ-----CVDLGSY 434
Db 757 NKGTVCQEKARPHCLCPPGWDGAYCDVLNVSKAALQKGVPEHLCQHSIGICINAGNTH 816
QY 435 ICQCAQFTGRHCDNDVDCASFPVCVNGGTCDQGVNDYSCTCPPGYNGKNCSTPVSRCEH 494
Db 817 HCQCPGLGYTGSYCEEQDECASNPCHOHATCNDFIGGYRCECVPGYQGVNCEYVEDECQN 876
QY 495 NPCXNGATCHERSNRVYVCECARGYGGLNCQFLLPEPPQGP 534
Db 877 QPCQNGGTCIDLNVHFKSCPPGTRGLLCEENIDECAGGP 916
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Search completed: November 29, 2004, 13:26:58
Job time : 22.2447 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:12:09 ; Search time 87.6462 Seconds
(without alignments)
4779.132 Million cell updates/sec

Title: US-09-783-931-2
Perfect score: 4153
Sequence: 1 MGRFLLTALLSALLCRQ.....YQSVVISEKDECIATEV 728

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4153	100.0	728	2	Q90656 gallus gall
2	3495.5	84.2	721	2	Q91902 xenopus lae
3	3487.5	84.0	723	1	DLL1 HUMAN
4	3449.5	83.1	726	2	Q9AW87 cynops pyrr
5	3410	82.1	722	2	Q6PFV7 mus musculu
6	3410	82.1	722	2	AAR57400 mus muscu
7	3410	82.1	722	2	AAR30869 mus muscu
8	3410	82.1	722	2	AAR65063 mus muscu
9	3407	82.0	722	1	DLL1 MOUSE
10	3354	80.8	714	1	DLL1_RAT
11	3064.5	73.8	720	2	Q8UW34 brachydanio
12	3061.5	73.7	717	2	P87357 brachydanio
13	2918.5	70.3	772	2	Q6DI48 brachydanio
14	2854.5	68.7	802	2	O57462 brachydanio
15	1945	46.8	642	2	Q7ZXT4 xenopus lae
16	1939	46.7	642	2	P79941 xenopus lae
17	1925.5	46.4	664	2	Q9IAT6 brachydanio
18	1897	45.7	685	1	Q9N161 homo sapien
19	1868	45.0	686	1	DLL4_HUMAN
20	1863	44.9	686	2	Q9DBU9 mus musculu
21	1852	44.6	615	2	O57409 mus musculu
22	1673	40.3	684	2	Q8I498 cupiennius
23	1560.5	37.6	833	2	Q8T4N0 drosophila
24	1560.5	37.6	833	2	Q6T4N6 drosophila
25	1560.5	37.6	833	2	AAR21453 drosophil
26	1560.5	37.6	833	2	AAR21462 drosophil
27	1560.5	37.6	833	2	AAR21463 drosophil
28	1559.5	37.6	833	1	DL DROME
29	1559.5	37.6	833	2	Q6T4N9 drosophila
30	1559.5	37.6	833	2	Q6T4N2 drosophila
31	1559.5	37.6	833	2	Q6T4N3 drosophila

32	1559.5	37.6	833	2	Q6T4N4 drosophila
33	1559.5	37.6	833	2	Q6T4N6 drosophila
34	1559.5	37.6	833	2	AAO25024 drosophil
35	1559.5	37.6	833	2	AAR21454 drosophil
36	1559.5	37.6	833	2	AAR21455 drosophil
37	1559.5	37.6	833	2	AAR21456 drosophil
38	1559.5	37.6	833	2	AAR21457 drosophil
39	1559.5	37.6	833	2	AAR21458 drosophil
40	1559.5	37.6	833	2	AAR21459 drosophil
41	1559.5	37.6	833	2	AAR21460 drosophil
42	1559.5	37.6	833	2	AAR21461 drosophil
43	1559.5	37.6	833	2	AAR21464 drosophil
44	1559.5	37.6	833	2	AAR21465 drosophil
45	1559.5	37.6	833	2	AAR21466 drosophil

ALIGNMENTS

RESULT 1
Q90656 PRELIMINARY; PRT; 728 AA.
AC Q90656;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE C-Delta-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=95319507; PubMed=7596411;
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the chick."
RL Nature 375:787-790(1995).
DR EMBL; U26590; AAC59689.1; -.
DR PIR; I50719; I50719.
DR HSP; P00740; LEDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR00152; Aex_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00068; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 728 AA; 79861 MW; 93B2D666DD2388B7 CRC64;

Query Match 100.0%; Score 4153; DB 2; Length 728;

Best Local Similarity 100.0%; Pred. No. 3.6e-268;

Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRFLLTALLSALLCRQVDGSGVPELKLQEFVNKKGLLSNRNCCRGSGGAGGQOC 60

Db 1 MGRFLLTALLSALLCRQVDGSGVPELKLQEFVNKKGLLSNRNCCRGSGGAGGQOC 60

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QY 61 DCKTFRVCLKHVQASVSPBPCTYGSALTVPVLGANSFSPVDPGAGDPAFNPPIRFPFG 120
Db 61 DCKTFRVCLKHVQASVSPBPCTYGSALTVPVLGANSFSPVDPGAGDPAFNPPIRFPFG 120
QY 121 FTWPGTFSLIIEALHTDSDDLTNTENPERLISRLATQRHLAVGEWSQDLHSSGRDLDKY 180
Db 121 FTWPGTFSLIIEALHTDSDDLTNTENPERLISRLATQRHLAVGEWSQDLHSSGRDLDKY 180
QY 181 SYRFVCDHYHGGCVSFCRPRDDRGHFTCGERGKVCNPNWKGQYCTEPICLPGCDBQ 240
Db 181 SYRFVCDHYHGGCVSFCRPRDDRGHFTCGERGKVCNPNWKGQYCTEPICLPGCDBQ 240
QY 241 HGFCDPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYCT 300
Db 241 HGFCDPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNYCT 300
QY 301 HHKPKCNKGATCTNTGQSYTCSRPGYTGSCEIEINECDANPCNKGSCCTDLENSYCT 360
Db 301 HHKPKCNKGATCTNTGQSYTCSRPGYTGSCEIEINECDANPCNKGSCCTDLENSYCT 360
QY 361 CPPGFYGNKCNLSAMTCADGCPFNCRGRTDNDPGGYSRCPLGYSGFNCEKKIDYCSSP 420
Db 361 CPPGFYGNKCNLSAMTCADGCPFNCRGRTDNDPGGYSRCPLGYSGFNCEKKIDYCSSP 420
QY 421 CANGAQCVDLGNYSYICQCOAGFTGRHCDNDVDDCASFPVCVNGSTCQDGVNDYSCTCPGY 480
Db 421 CANGAQCVDLGNYSYICQCOAGFTGRHCDNDVDDCASFPVCVNGSTCQDGVNDYSCTCPGY 480
QY 481 NGKNCSTPVSRCHEHNPCHNGATCHEHSRNYRVECEARGYGLNCQFLPPPGQPVVDFT 540
Db 481 NGKNCSTPVSRCHEHNPCHNGATCHEHSRNYRVECEARGYGLNCQFLPPPGQPVVDFT 540
QY 541 EKYTEGQNSQFPWIAVCAGIILVLLMLLGCALIVVCRLKVKQRHHQHPACRSSETETMNN 600
Db 541 EKYTEGQNSQFPWIAVCAGIILVLLMLLGCALIVVCRLKVKQRHHQHPACRSSETETMNN 600
QY 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVDYNLVHELKNEDSV 660
Db 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVDYNLVHELKNEDSV 660
QY 661 KEEHGKCEAKCETDYSEAEKSAVQLKSSDTSERKRPSDVSYSTKDYQSVYVISEEK 720
Db 661 KEEHGKCEAKCETDYSEAEKSAVQLKSSDTSERKRPSDVSYSTKDYQSVYVISEEK 720
QY 721 ECIIATEV 728
Db 721 ECIIATEV 728

RESULT 2
Q91902 PRELIMINARY; PRT; 721 AA.
AC Q91902;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE X-Delta-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
OC Xenopodinae; Xenopus.
OX NCB_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319507; PubMed=7596411;
RA Henrique D., Adam J., Mvat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the
RT chick.";
RL Nature 375:787-790(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319503; PubMed=7596407;
RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
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RT "Primary neurogenesis in Xenopus embryos regulated by a homologue of
RT the Drosophila neurogenic gene Delta.";
RL Nature 375:761-766(1995).
DR EMBL; L42229; AAC38017.1; -.
DR HSSP; P00740; C:membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; A:cell communication; IEA.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF II.
DR InterPro; IPR001438; EGF I.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFALOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 721 AA; 79922 MW; 9BDC85C439DD194 CRC64;

Query Match 84.2%; Score 3495.5; DB 2; Length 721;
Best Local Similarity 82.2%; Pred. No. 2.1e-224;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;

QY 1 MGRFLLTALLSALLCRCQVDGSGVFELKLOEFVFNKGLLSNRNCCRGGGPGG-AGQQQ 59
Db 1 MGQRMFLTLVLSAVL--CQISCSGLFELRLQEFVFNKGLLGNMNCRC--PGSLASLQ 55
QY 60 CDCKTFFRVCLKHVQASVSPBPCTYGSALTVPVLGANSFSPVDPGAGDPAFNPPIRFP 119
Db 56 CECKTFFRCLKHVQSNVSPBPCTYGGAVPVLGNSFVVP-SSNADPTSNPIRFP 114
QY 120 QTWPGTFSLIIEALHTDSDDLTNTENPERLISRLATQRHLAVGEWSQDLHSSGRDLDK 179
Db 115 GTPWPGTFSLIIEATHADSADLTNTENPERLISRLATQRHLTVGRQWSQDLHSSDRT 174
QY 180 YSYRFVCDHYHGGCVSFCRPRDDRGHFTCGERGKVCNPNWKGQYCTEPICLPGCDB 239
Db 175 YSYRFVCDHYHGGCVSFCRPRDDRGHFTCGERGKVCNPNWKGQYCTEPICLPGCDB 234
QY 240 QHGFCDKPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNY 299
Db 235 HHGYCDKPGCKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNCQEGWGLFCNQDLNY 294
QY 300 THHKPKCNKGATCTNTGQSYTCSRPGYTGSCEIEINECDANPCNKGSCCTDLENSYSC 359
Db 295 THHKPCENGATCTNTGQSYTCSRPGYTGSCEIEINECDANPCNKGSCSDLENSYTC 354
QY 360 TCPPGFYGNKCNLSAMTCADGCPFNCRGRTDNDPGGYSRCPLGYSGFNCEKKIDYCSS 419
Db 355 SCPPGFYGNKCNLSAMTCADGCPFNCRGRTDNDPGGYSRCPLGYSGFNCEKKIDYCSS 414
QY 420 PCANGAQCVDLGNYSYICQCOAGFTGRHCDNDVDDCASFPVCVNGSTCQDGVNDYSC 479
Db 415 PCANGARCEDLGNYSYICQCOAGFTGRHCDNDVDDCASFPVCVNGSTCQDGVNDYSC 474
QY 480 YNGKNCSTPVSRCHEHNPCHNGATCHEHSRNYRVECEARGYGLNCQFLPPPGQPVVD 539
Db 475 YIGKNCSPITKCEHNPCHNGATCHEHSRNYRVECEARGYGLNCQFLPP-EPKVVVDL 532
QY 540 TEKYTEGQNSQFPWIAVCAGIILVLLMLLGCALIVVCRLKVKQRHHQHPACRSSET 599
Db 533 TEKYTEGQSGQFPWIAVCAGIILVLLMLLGCALIVVCRLKVKQRHHQHPACRGSKTN 592
QY 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSD-NSDKNGYKVRYPVDYNLVHELKNE 658
Db 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSD-NSDKNGYKVRYPVDYNLVHELKNE 658
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[illegible]


```
QY 240 QHGFCDKPGCKCRVWGQGRYDCBCIRYPGCLHGTCCQPPWQCNCQBGWGLFCNODLNYC 299
Db 232 QHGFCDKPGCKCRVWGQGRYDCBCIRYPGCLHGTCCQPPWQCNCQBGWGLFCNODLNYC 291
QY 300 THHKPCNGKATCTNTQGGSYTCSCRPYTGSSCEIBEINECDANPCKNKGSCSTDLENSYSC 359
Db 292 THHKPCNGKATCTNTQGGSYTCSCRPYTGANCELEVEDECAPSPCKNGASCSTDLEDSFSC 351
QY 360 TCPPGYGKNCBELSAMTCADGPCFNGGRTDNDPDDGYSRCPLGYSGFNCEKIDYCSSS 419
Db 352 TCPPGYGKNCBELSAMTCADGPCFNGGRCSDNDPDDGYSRCPLGYSGFNCEKIDYCSSS 411
QY 420 PCANGAACVDLGNYSYTCQAGFTGRHCDNDVDDCASFCVNGGTCQDGVNDYSCTCPPG 479
Db 412 PCANGAACVDLGNYSYTCQAGFTGRHCDNDVDDCASFCVNGGTCQDGVNDYSCTCPPG 471
QY 480 YNGKNCSTPVSRCENHPCNGATCHERSNRYVCECARGYGGNLCQFLLPEPPGQPVVDF 539
Db 472 YTGKNCSTPVSRCENHPCNGATCHERSNRYVCECARGYGGNLCQFLLPEPPGQPVVDF 531
QY 540 THKYTEGQNSQPPWIAVACAGIILVLLMLLGCRAIVVCRVLKVKRHHQPEACRSETETWN 599
Db 532 SERHMSQGGPPFWAVACAGIILVLLMLLGCRAIVVCRVLKVKRHHQPEACRSETETWN 591
QY 600 NLANCOREKXIDISTSVIGATQIKNTNKKVDFHSDN-SDKNKYKVRYPVSDYNLVHELK-NE 657
Db 592 NLANCOREKXIDISTSVIGATQIKNTNKKVDFHSDN-SDKNKYKVRYPVSDYNLVHELK-NE 651
QY 658 DSVKEHKGCEAKCTYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVYLSA 717
Db 652 ATVRDTHSKRDTKQCSQSSAGEEKIAPTRLGGEIPDRKRPESVYSTSKDTKYQSVVYLSA 711
QY 718 EKDECVIATEV 728
Db 712 EKDECVIATEV 722

RESULT 6
AAH57400 PRELIMINARY; PRT; 722 AA.
AC AAH57400;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Delta-like 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]_
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skala U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

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[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057400; AAH57400.1; -.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 82.1%; Score 3410; DB 2; Length 722;
Best Local Similarity 79.5%; Pred. No. 1.1e-218;
Matches 581; Conservative 72; Mismatches 66; Indels 12; Gaps 6;

QY 1 MGRFLLTLLALSLALCRCONVDSGVFEELKLEFVFNKGLLSNRNCCRG-CPGAGAQOQ 59
Db 1 MGRFLLTLLALSLALCRCONVDSGVFEELKLEFVFNKGLLSNRNCCRGSP-----P 52
QY 60 CDCKTFRRVCLKHYSVPEPPCTYGSAITPVLGANSFSPVPGAGGADPAFSPNIRPFP 119
Db 53 CACRTFFRVCLKHYSVPEPPCTYGSAITPVLGANSFSPVPGAGGADPAFSPNIRPFP 111
QY 120 GFTWPGTSLIIEALHTSDPDLTTENPERLISRLATQRIHLAVGEWSQDLHSSGRTDLK 179
Db 112 GFTWPGTSLIIEALHTSDPDLTTENPERLISRLATQRIHLAVGEWSQDLHSSGRTDLR 171
QY 180 YSYRFVCDHEHYGECVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDB 239
Db 172 YSYRFVCDHEHYGECVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDD 231
QY 240 QHGFCDKPGCKCRVWGQGRYDCBCIRYPGCLHGTCCQPPWQCNCQBGWGLFCNODLNYC 299
Db 232 QHGFCDKPGCKCRVWGQGRYDCBCIRYPGCLHGTCCQPPWQCNCQBGWGLFCNODLNYC 291
QY 300 THHKPCNGKATCTNTQGGSYTCSCRPYTGSSCEIBEINECDANPCKNKGSCSTDLENSYSC 359
Db 292 THHKPCNGKATCTNTQGGSYTCSCRPYTGANCELEVEDECAPSPCKNGASCSTDLEDSFSC 351
QY 360 TCPPGYGKNCBELSAMTCADGPCFNGGRTDNDPDDGYSRCPLGYSGFNCEKIDYCSSS 419
Db 352 TCPPGYGKNCBELSAMTCADGPCFNGGRCSDNDPDDGYSRCPLGYSGFNCEKIDYCSSS 411
QY 420 PCANGAACVDLGNYSYTCQAGFTGRHCDNDVDDCASFCVNGGTCQDGVNDYSCTCPPG 479
Db 412 PCANGAACVDLGNYSYTCQAGFTGRHCDNDVDDCASFCVNGGTCQDGVNDYSCTCPPG 471
QY 480 YNGKNCSTPVSRCENHPCNGATCHERSNRYVCECARGYGGNLCQFLLPEPPGQPVVDF 539
Db 472 YTGKNCSTPVSRCENHPCNGATCHERSNRYVCECARGYGGNLCQFLLPEPPGQPVVDF 531
QY 540 TEKYTEGQNSQPPWIAVACAGIILVLLMLLGCRAIVVCRVLKVKRHHQPEACRSETETWN 599
Db 532 SERHMSQGGPPFWAVACAGIILVLLMLLGCRAIVVCRVLKVKRHHQPEACRSETETWN 591
QY 600 NLANCOREKXIDISTSVIGATQIKNTNKKVDFHSDN-SDKNKYKVRYPVSDYNLVHELK-NE 657
Db 592 NLANCOREKXIDISTSVIGATQIKNTNKKVDFHSDN-SDKNKYKVRYPVSDYNLVHELK-NE 651
QY 658 DSVKEHKGCEAKCTYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVYLSA 717
Db 652 ATVRDTHSKRDTKQCSQSSAGEEKIAPTRLGGEIPDRKRPESVYSTSKDTKYQSVVYLSA 711
QY 718 EKDECVIATEV 728
Db 712 EKDECVIATEV 722

RESULT 7
AAH30869 PRELIMINARY; PRT; 722 AA.
AC AAH30869;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Delta like-1.
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Db 292 THHKPCRNGATCTNTQGGSYTCSCRPYTGANCELEVDCAEPCPKNGKASCTDLEDFSC 351
Qy 360 TCPPGYGKNCELSAMTCADGCPGNGRCRTDNDPGYSRCPLGYSGFNCCKIDYCS 419
Db 352 TCPPGYGKNCELSAMTCADGCPGNGRCSDNDPGYTCHPLGYSGFNCCKMDLCS 411
Qy 420 PCANGAQCVDLGNYSYTCQAGFTGRHCDNDVDCCASFPVCVNGTCCDGVNDYSCTCP 479
Db 412 PCNGAKCVDLGNYSYLCRQAGSGRGCECDNDVDCCASSPANGGTCRDVNDYSCTCP 471
Qy 480 YNGKNCSTPVSRCHEPNCHNGATCHERSNRYVCECARGYGGNLCQFLLEPPPGQ 539
Db 472 YTGKNCAPVSRCEHAPCHNGATCHQGRQRYMCECAQYGGNLCQFLLEPPPGQ 531
Qy 540 TEKYTGQNSQPMIACVAGIILVLLGCAIIVCVRLKVQKRHHQPEACRSETETWN 599
Db 532 SERHMSQGGPPFWAVACGVVLVLLGCAVYVVRVRLKQKHQPPPECGGETETWN 591
Qy 600 NLANCOREKDISVIGATQIKNTNKKVDPHSDN-SDKNGYKVRYPVDYNLVHELK-NE 657
Db 592 NLANCOREKDVSVIIGATQIKNTNKKADPHGDHGAESKFRKYRYPVDYNLVRLD 651
Qy 658 DSVKEHGKCEAKCETYDSEAEKSAVOLKSDTSERKRPDSVYSTSKDTKYQSVV 717
Db 652 ATVRDTHSKRDTKQSQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSV 711
Qy 718 EKDECIATEV 728
Db 712 EKDECVIATEV 722

RESULT 9
DL11_MOUSE
ID DL11_MOUSE STANDARD; PRT; 722 AA.
AC Q61483;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
GN Name=Dll1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;
RA Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
RT "Transient and restricted expression during mouse embryogenesis of
RL Dll1, a murine gene closely related to Drosophila Delta.";
CC -!- FUNCTION: May be involved in cell-to-cell communication in
CC mammalian embryos. May have a role in cellular interactions
CC underlying somitogenesis and development of the nervous system.
CC -!- SUBUNIT: Interacts with Notch receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In the embryo, expressed in the paraxial
CC mesoderm and nervous system. Expressed at high levels in adult
CC heart and at lower levels, in adult lung.
CC -!- DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo.
CC Expression then decreases and increases again in the adult.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR BMBL; X80903; CAA56865.1; -.
DR PIR; I48324; I48324.
DR HSP; P00740; IEDM.
DR IntAct; Q61483; -.
DR MGD; MGI:104659; Dll1.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005113; F:Notch binding; IPI.
DR GO; GO:0005513; F:protein binding; IPI.
DR GO; GO:0001709; P:cell fate determination; ISS.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
DR GO; GO:0009113; P:hair cell fate commitment; NAS.
DR GO; GO:0030097; P:hemoiesis; ISS.
DR GO; GO:0042472; P:inner ear morphogenesis; NAS.
DR GO; GO:0007399; P:neurogenesis; NAS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); NAS.
DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 722 Delta-like protein 1.
FT DOMAIN 18 545 Extracellular (Potential).
FT TRANSMEM 546 568 Potential.
FT DOMAIN 569 722 Cytoplasmic (Potential).
FT DOMAIN 158 220 DSL.
FT DOMAIN 225 253 EGF-like 1.
FT DOMAIN 256 284 EGF-like 2.
FT DOMAIN 291 324 EGF-like 3.
FT DOMAIN 331 362 EGF-like 4.
FT DOMAIN 369 401 EGF-like 5.
FT DOMAIN 408 439 EGF-like 6.
FT DOMAIN 446 477 EGF-like 7.
FT DOMAIN 484 515 EGF-like 8.
FT DISULFID 225 236 By similarity.
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FT DISULFID 430 439 By similarity.
FT DISULFID 446 466 By similarity.
FT DISULFID 468 477 By similarity.
FT DISULFID 484 495 By similarity.
FT DISULFID 489 504 By similarity.
FT DISULFID 506 515 By similarity.

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FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 722 AA; 78448 MW; 95F581B56DCEC980 CRC64;
Query Match 82.0%; Score 3407; DB 1; Length 722;
Best Local Similarity 79.5%; Pred. No. 1.7e-218; Indels 12; Gaps 6;
Matches 581; Conservative 71; Mismatches 67;
Qy 1 MGRFLTLALLSALLCRQVDGSGVFELKQLQEFVNNKGLLSNRNCRGG-GPGAGGQQQ 59
Db 1 MGRSALALAVVSALL--CQWSSGVFELKQLQEFVNNKGLLSNRNCRGGSGP-----P 52
Qy 60 CDCTFFRVCLKHQVQASVPEPPCTYSATIPVLGANSFSDPGAGGADPAFSPPIRPPF 119
Db 53 CACRTFFRVCLKHQVQASVPEPPCTYSATIPVLGANSFSDPGAGGADPAFSPPIRPPF 111
Qy 120 GFTWPGFSLIIEALHTDSDLTENPERLISRLATORHLAVGEWSQDLHSSGRTDLK 179
Db 112 GFTWPGFSLIIEALHTDSDLTENPERLISRLATORHLAVGEWSQDLHSSGRTDLK 171
Qy 180 YSYRFVCDHYHGECSVFCRPRDRFGHCTGGERGEKVCNPGWKQGYCTEPICLPGCDE 239
Db 172 YSYRFVCDHYHGECSVFCRPRDRFGHCTGGERGEKVCNPGWKQGYCTEPICLPGCDD 231
Qy 240 QHGCDRPECKCRVWQGRYCDICIRYPGCLHGTCCQPMWCNCOBGGGLFCNQDLNYC 299
Db 232 QHGCDRPECKCRVWQGRYCDICIRYPGCLHGTCCQPMWCNCOBGGGLFCNQDLNYC 291
Qy 300 THHPCKNGATCTNTGQSGSYTCRPGVTGSSCEIENECNANCKNGSGCTDLENSVSC 359
Db 292 THHPCKNGATCTNTGQSGSYTCRPGVTGSSCEIENECNANCKNGSGCTDLENSVSC 351
Qy 360 TCPFGFYKNCELSAMTCADGCFNGRCRTDNPGGYSCRCPLGYSGFNCCKKIDYCSSS 419
Db 352 TCPFGFYKNCELSAMTCADGCFNGRCRTDNPGGYSCRCPLGYSGFNCCKKIDYCSSS 411
Qy 420 PCANGACVDLGNYSYICOCQAGFTGRHCDNDVDCASFPVNGGTCDQGVNDYSCTCPPG 479
Db 412 PCSNGAKCVDLGNYSYICOCQAGFTGRHCDNDVDCASFPVNGGTCDQGVNDYSCTCPPG 471
Qy 480 YNGKNCSTPVSRCHNPNCHGATCHERSNRVVCRCARGYGLNCOFLPEPPQGVLVDF 539
Db 472 YTGKNCSTPVSRCHNPNCHGATCHERSNRVVCRCARGYGLNCOFLPEPPQGVLVDF 531
Qy 540 TEKYTEGNSOPFPIAVCAGIILMLLLGCAAVVLCVLRKVRHHPQACREGETETMN 599
Db 532 SERHESQGGPPPVAVCAGIILMLLLGCAAVVLCVLRKVRHHPQACREGETETMN 591
Qy 600 NLANCOREKDISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPVSDYNLHKLK-NE 657
Db 592 NLANCOREKDISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPVSDYNLHKLK-NE 651
Qy 658 DSVKEEHCKCAKCTYDSEAEKSAVOLKSSDTSEKRPDSVYSTKDTKYQSVYVISE 717
Db 652 ATVTDTHSKRTKQOSOSAGEEKIAPLRGGEIPDRKRPSVYSTKDTKYQSVYVISA 711
Qy 718 EKDECIATEV 728
Db 712 EKDECIATEV 722
RESULT 10
ID DLI1 RAT STANDARD; PRT; 714 AA.
AC P9767;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta).
GN Name=DLL1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

FN SEQUENCE FROM N.A.
RA Disibio G., Hebehi L., Boulter J., Weinmaster G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in cell-to-cell communication in
CC mammalian embryos. May have a role in cellular interactions
CC underlying somitogenesis and development of the nervous system (By
CC similarity).
CC -!- SUBUNIT: Interacts with Notch receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch.
CC -----
CC EMBL; U78889; AAB37343.1; -;
CC HSSP; P08709; 1B99.
CC RGD; 70949; D111.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005112; F:Notch binding; IPI.
CC GO; GO:0001154; P:cell differentiation; ISS.
CC GO; GO:0001701; P:cell fate determination; ISS.
CC GO; GO:0001709; P:embryonic development (sensu Mammalia); ISS.
CC GO; GO:000912; P:hair cell fate commitment; NAS.
CC GO; GO:0030097; P:hemopoiesis; ISS.
CC GO; GO:0042472; P:inner ear morphogenesis; ISS.
CC GO; GO:0007399; P:neurogenesis; NAS.
CC GO; GO:0007219; P:Notch signaling pathway; NAS.
CC GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
CC GO; GO:0030155; P:regulation of cell adhesion; ISS.
CC InterPro; IPR00152; Aax hydroxyl_S.
CC InterPro; IPR01774; DSL.
CC InterPro; IPR00742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF_Like.
CC Pfam; PF01414; DSL; 1.
CC Pfam; PF00008; EGF; 6.
CC PRINTS; PR0010; EGFBL00.
CC SMART; SM00051; DSL; 1.
CC SMART; SM00179; EGF_CA; 4.
CC PROSITE; PS00010; ASX_HYDROXYL; 3.
CC PROSITE; PS00022; EGF_1; 8.
CC PROSITE; PS01186; EGF_2; 8.
CC PROSITE; PS50026; EGF_3; 7.
CC PROSITE; PS01187; EGF_CA; 2.
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 714 Delta-like protein 1.
FT DOMAIN 18 537 Extracellular (Potential).
FT TRANSMEM 538 560 Potential.
FT DOMAIN 561 714 Cytoplasmic (Potential).
FT DOMAIN 158 220 DSL.
FT DOMAIN 225 253 EGF-like 1.
FT DOMAIN 256 284 EGF-like 2.
FT DOMAIN 291 324 EGF-like 3.
FT DOMAIN 331 362 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 369 401 EGF-like 5.
FT DOMAIN 406 439 EGF-like 6.
FT DOMAIN 446 477 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 484 515 EGF-like 8.
FT DISULFID 225 236 By similarity.
FT DISULFID 229 242 By similarity.
FT DISULFID 244 253 By similarity.
FT DISULFID 256 267 By similarity.

FT	DISULFID	262	273	By similarity.
FT	DISULFID	275	284	By similarity.
FT	DISULFID	291	303	By similarity.
FT	DISULFID	297	313	By similarity.
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FT	DISULFID	408	419	By similarity.
FT	DISULFID	413	428	By similarity.
FT	DISULFID	430	439	By similarity.
FT	DISULFID	446	466	By similarity.
FT	DISULFID	468	477	By similarity.
FT	DISULFID	484	495	By similarity.
FT	DISULFID	489	504	By similarity.
FT	DISULFID	506	515	By similarity.
FT	CARBOHYD	476	476	N-linked (GlcNAc...) (Potential).
SQ	SEQUENCE	714 AA;	77378 MW; 488E2272BAEA27E CRC64;	
Query Match 80.8%; Score 3354; DB 1; Length 714;				
Best Local Similarity 78.4%; Pred. No. 5.6e-215;				
Matches 573; Conservative 69; Mismatches 69; Indels 20; Gaps 7;				
QY	1	MGRFLLTALLSALLCRCQVDGSGVFELKQBFVNKGLLSNRNCRGG-GPGGAGQQQ	59	
DB	1	MGRSSALAVVALL--CQVSSGVFELKQBFVNKGLLSNRNCRGGSGP-----P	52	
QY	60	CDCKTFRVLKHQASVSEPPCTYGSATIPVLGANSFVDPDGAGADPAFNSPIRFPF	119	
DB	53	CACRTFRVLKHQASVSEPPCTYGSATVAVLGVDSFSLPDGA-GIDPAFNSPIRFPF	111	
QY	120	GFTWPGTFFSLIEALHTSDPDDLTTENPERLISRLATQRLAVGEWSQDLHSSGRTDLK	179	
DB	112	GFTWPGTFFSLIEALHTSDPDDLATTENPERLISRLTQRLHVTGEWSQDLHSSGRTDLR	171	
QY	180	YSYRFVCDHYHGECSVFCRPRDRFQHTFCGERGEKVCNPGWKQYCTEPICLPGDCE	239	
DB	172	YSYRFVCDHYHGECSVFCRPRDDAFQHTFCGERGEKVCNPGWKQYCTDPICLPGCDD	231	
QY	240	QHGFCDKPECKRQVQWQRYDECIYRPGCLHGTQQPWCNQCQBGWGLFCNQDLNYC	299	
DB	232	QHGFCDKPECKRQVQWQRYDECIYRPGCLHGTQQPWCNQCQBGWGLFCNQDLNYC	291	
QY	300	THHKPCNKATCTNTQGSYTCSCRPYTGSSCEIBEINCDANPCNKGSGCTDLENSYSC	359	
DB	292	THHKPCNKATCTNTQGSYTCSCRPYTGANCELEVEDECAPCRNGSGCTDLEDSYSC	351	
QY	360	TCPPGPGYKNCBELSAMTCADGCFNGGRTDNDPGYSCBPLGYSGFNCBKKIDYCSSS	419	
DB	352	TCPPGPGYKVCBELSAMTCADGCFNGGRCSDNDPGYTCCHPAGFSGFNCBKKIDYCSSS	411	
QY	420	PCANGAQCVDLGNYSYCQAGFTGRHCDNDVDDCASFPVCNNGTCCDGVNDYSCTCPBG	479	
DB	412	PCSGNAKQVDLGNYSYLCRCQTGFSGRYCBNDVDDCASFPANGGTCDSDVNDYSCTCPBG	471	
QY	480	YNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGGLNCQFLLPEPPQGVINDF	539	
DB	472	YTGRCNSAPVSRCEHAPCHNGATCHQRGQRYWCECAQYGGGANGCQFLLPEPPDPLIVA--	529	
QY	540	TEKYTEGQNSQFPWIAVAGAILVLLMLLGCAAIVCVRLKVQKRHHQPEACRSETETWN	599	
DB	530	-----AQGGSPFWAVAGVLLVLLLLGCAAVVVVRVRLKLQKHQPPDPDPCGGETETWN	583	
QY	600	NLANCOREKDISISVIGATQIKNTNKKVDFHSDN--SDKNGYKRVYPSVDYNLVHELK-NE	657	
DB	584	NLANCOREKDVSVIIGATQIKNTNKKADFHGDHGAADKSSFKARYPTVDYNLIRLDKGE	643	
QY	658	DSYKEBHGKCAKETYDSEAEKSAVOLKSDSTSRKRPDSYISTSKDTKYQSVYVISE	717	
DB	644	ATVRDAHSKRDTKCQSQSGSVGEKSTSLTRGGEVDPDRKRPESVYSTSKDTKYQSVYVLSA	703	

QY	718	EKDECIATEV	728	
DB	704	EKDECVIATEV	714	
RESULT 11				
Q8UWJ4		PRELIMINARY;	PRT;	720 AA.
ID	Q8UWJ4;			
AC	Q8UWJ4;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	DeltaD protein.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]_TaxID=7955;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22248969; PubMed=12361969;			
RA	Hans S., Campos-Ortega J.A.;			
RT	"On the organisation of the regulatory region of the zebrafish deltaD			
RT	gene.";			
RL	Development 129:4773-4784(2002).			
DR	EMBL; AF426384; AAL31528.1; -.			
DR	HSSP; P00740; IEDM.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0007154; P:cell communication; IEA.			
DR	InterPro; IPR000152; Asx_hydroxyl_S.			
DR	InterPro; IPR001774; DSL.			
DR	InterPro; IPR000742; EGF 2.			
DR	InterPro; IPR001881; EGF Ca.			
DR	InterPro; IPR001438; EGF II.			
DR	InterPro; IPR006209; EGF_like.			
DR	Pfam; PF01414; DSL; 1.			
DR	Pfam; PF00008; EGF; 6.			
DR	PRINTS; PR00010; EGFLOOD.			
DR	SMART; SM00051; DSL; 1.			
DR	SMART; SM00179; EGF CA; 4.			
DR	PROSITE; PS00010; ASX HYDROXYL; 3.			
DR	PROSITE; PS00022; EGF_1; 8.			
DR	PROSITE; PS01186; EGF_2; 8.			
DR	PROSITE; PS00026; EGF_3; 6.			
DR	PROSITE; PS01187; EGF_CA; 2.			
KW	EGF-like domain.			
SQ	SEQUENCE 720 AA; 79380 MW; DE6B7393E2AA0FE6 CRC64;			
Query Match 73.8%; Score 3064.5; DB 2; Length 720;				
Best Local Similarity 73.3%; Pred. No. 1.1e-195;				
Matches 531; Conservative 81; Mismatches 95; Indels 17; Gaps 11;				
QY	11	LLSALLRCQVDG--SGVFELKQBFVNKGLLSNRNCRGGGPGAGQQQCDCKTFPRV	68	
DB	5	MIAVLVCWISQGFCSGVFELKQBFVNKGLLVGTGNANCKGSAAG--HQECKTFPRV	61	
QY	69	CLKHYQASVSEPPCTYGSATIPVLGANSFVDPDGAGADPAFNSPIRFPFGTWPGTFS	128	
DB	62	CLKHYQANVSDPPCTYGGAVTFLGNSNFQVDSF--PDSFTNPFPFAGFTWPGTFS	119	
QY	129	LIIEALHTSDPDDLTTENPERLISRLATQRLAVGEWSQDLHSSGRTDLKYSYRFVCDCE	188	
DB	120	LIIEALHTSDDDLSTENPDRLSRMTTQRLHVTGEWSQDLQVGRTELKYSYRFVCDCE	179	
QY	189	HYYGSGCVFCRPRDRFQHTFCGERGEKVCNPGWKQYCTEPICLPGDCEHQFCDKPG	248	
DB	180	HYYGSGCVFCRPRDRDTQHTFCGERGEIICNSHWGQYCTEPICLPGDCEHQFCDKPG	239	
QY	249	ECKCRVWGQRYDCIRYPGCLHGTCCQPPWCNQCQBGWGLFCNQDLNYCTHHKPCQNG	308	
DB	240	ECKCRVSGKYCDDCIRYPGCLHGTCCQPPWCNQCQBGWGLFCNQDLNYCTHHKPCQNG	299	

Qy	309	ATCNTNGSGSYTCSRPGYTGSSCEIENECDANPCNKGSCSTDLENSYSCTCPGPGFYGR	368
Dd	300	: : : : : : : : : :	
Qy	369	NCELSAMTCADGPCFNGRCRTDNPDGGYSCRPLGYSGFNCBKKIDYCSSSPCANGAQCVC	428
Dd	360	: : : : : : : : :	
Qy	429	DLGNSYICOCQAAGFTGRHCDNDVDCAFPCCVNGGTCCDGVNDYSCTCPPGYNGKNCSTP	488
Dd	420	: : : : : : : : :	
Qy	489	VSRCHNPCHNGATCHERSNRNYVCCARGYGGLNCQFLPPBPQPQGPVIUDFTEK-YT-BG	546
Dd	480	: : : : : : : : :	
Qy	547	QNSOFFPWTAACAGIILMLLLGCAAIVVVRVLKVQRKHQPEACRSETETMNNLANCO-	605
Dd	540	: : : : : : : : :	
Qy	606	REKDISISVIGATQIKNTNKVKVDPHSDNSDKNGYKRVYPVDVNLVHELKNEDSVKEEHG	665
Dd	599	: : : : : : : : :	
Qy	666	KCEA-KCETYDSEABEKSAVOLKSSDTSERKRPSDYSTS KDTKYQS VYVISEEKDECI I	724
Dd	658	: : : : : : : : : :	
Qy	725	RSEATKCEPLDSDBEAKRHNLK-SDSSEKRKTESL---CKDTKYQS FVLSEKDECI I	713
Dd	714	AEEV 728 : ATEI 717	
RESULT 12			
P87357	ID	P87357 PRELIMINARY; PRT; 717 AA.	
AC	P87357;		
DT	01-MAY-1997 (TrEMBLrel. 03, Created)		
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Delta d transmembrane protein precursor.		
GN	Name=dld; Synonyms=delta d;		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97346722; PubMed=9203139;		
RA	Dornseifer P., Takke C., Campos-Ortega J.A.;		
RT	"Overexpression of a zebrafish homologue of the Drosophila neurogenic		
RT	gene delta perturbs differentiation of primary neurons and somitic		
RL	development.";		
RL	Mech. Dev. 63:159-171(1997).		
DR	EMBL; Y11760; CAA72425.1; -.		
DR	HSP; P00740; IEDM		
DR	ZFIN; ZDB-GENE-990415-47; dld.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0007154; P:cell communication; IEA.		
DR	InterPro; IPRO00152; Asx hydroxyl_S.		
DR	InterPro; IPRO01774; DSL_.		
DR	InterPro; IPRO00742; EGF_2.		
DR	InterPro; IPRO01881; EGF_Ca.		
DR	InterPro; IPRO01438; EGF_I1.		
DR	InterPro; IPRO06209; EGF_like.		
DR	Pfam; PF01414; DSL; 1.		
DR	Pfam; PF00008; EGF; 6.		
DR	PRINTS; PR00010; EGF_BLOOD.		
DR	SMART; SM00051; DSL; 1.		
DR	SMART; SM00179; EGF_CA; 4.		


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Query Match 68.7%; Score 2854.5; DB 2; Length 802;
Best Local Similarity 66.4%; Pred. No. 1.1e-181;
Matches 502; Conservative 78; Mismatches 123; Indels 53; Gaps 15;

QY 3 GRFLTLALLSALLCRQVDSGVFELKLOEFVNKGLLSNRNCRGGPGAGGQOQDC 62
DB 40 GRHLULLLFSILYMLLQASSGVFELKLOFLNKKGVGNKCKGLT--TSYQCEC 97
QY 63 KTFRVLCKHQASVPEPPCTYCSAITPVLGANSFSPDGGAGGADPAFSPNIPFPF 122
DB 98 KTFRVLCKHQASVPEPPCTYCSAITPVLGANSFSPDGGAGGADPAFSPNIPFPF 155
QY 123 WPGTFLSLIIEALHTSDPDLTENPERLISRLATORHLAVGEWSQDLHSGRTDLKYSY 182
DB 156 WPGTFLSLIIEALHADSKEIDLATENPERIISTMTTQHLTVGEDMSQDLHSGRTDLKYSY 215
QY 183 RFVDEHYHGGCVFCPRDRGHFTCGERGEKVCNPKHGKQYCTEPICLPGCDEOHG 242
DB 216 RFVDEHYHGGCVFCPRDRGHFTCGERGEKVCNPKHGKQYCTEPICLPGCDEOHG 275
QY 243 FCDKPGCKRCVGMQGRYCDICIRYPGCLHGTCTQCPWQCNCQEGWGLFCNQDNLNCTHH 302
DB 276 FCEKPGCKRCVGMQGRYCDICIRYPGCLHGTCTQCPWQCNCQEGWGLFCNQDNLNCTHH 335
QY 303 KPCXGATCTNTGSGSYTCRPGVTGSSGIEINECDANPCXGSGCTDLNYSYCTCP 362
DB 336 KPCXGATCTNTGSGSYTCRPGVTGSSGIEINECDANPCXGSGCTDLNYSYCTCP 395
QY 363 PGFYGNKCELSAMTADGCPFCNGRCCTDNPGGYSCRCPLGSGFNCCKTDYCSSPCA 422
DB 396 PGFYGNKCELSAMTADGCPFCNGRCCTDNPGGYSCRCPLGSGFNCCKTDYCSSPCA 455
QY 423 NGAOCVDLNSYICQOAGFTGRHCDNDVDCASFPVCNGGTCTDGVNDYSCCTPPGYNG 482
DB 456 NGAOCVDLNSYICQOAGFTGRHCDNDVDCASFPVCNGGTCTDGVNDYSCCTPPGYNG 515
QY 483 KNCSTPVSRCBHPCHNGATCHERNRYVCACVSGYGRNCQFLLPD--RASQIA---- 542
DB 516 KNCSTPVSRCBHPCHNGATCHERNRYVCACVSGYGRNCQFLLPD--RASQIA---- 568
QY 543 YTEGNSQFPNIAVCAGIILVLLGLLCAALVVCRLKQV--KRHHQPEACRSETMWN 600
DB 569 YTEGNSQFPNIAVCAGIILVLLGLLCAALVVCRLKQV--KRHHQPEACRSETMWN 622
QY 601 LA-NQCEKDISISVIGATQIKNTNKKVDPHSDNSD-----KNGYKVRVPSVDYNLVHE 653
DB 623 LTNNCHRDKDLAVSVGVAPVKNINKIDFSSDHDHLSLTTEKRSYKTRHAPADYNLVHE 682
QY 654 LKNE--DSVKEEH-GK-----CE-AKCTYDSEA---BEKSAVQLKSSDTSERK 695
DB 683 VKFEVKHEVLEHAGKETTANELSDSCEDIKCQSLQDSBCTEKKRKRKLKSDASESK 742
QY 696 RPDVSYSTSK--DTKYOSVYVISEK--DECIATFV 728
DB 743 YSERYSESKYSSEKY-----SESKYSRCAVAFV 772

RESULT 15
Q72XT4 PRELIMINARY; PRT; 642 AA.
AC Q72XT4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MG52561 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;

MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzanski M.I., Stalska U., Smailus D.E., Scherth A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative";
Dev. Dyn. 225:384-391(2002).
[3]
SEQUENCE FROM N.A.
TISSUE=Embryo;
Klein S.L., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC044262; AAH44262.1; -.
HSP; P00740; IEDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007154; P:cell communication; IEA.
InterPro; IPR000152; Aex_hydroxyl_S.
InterPro; IPR001774; DSL.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_like.
Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 5.
Pfam; PF07645; EGF_CA; 1.
PRINTS; PR00010; EGFBLD.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF_CA; 3.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF_1; 8.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS00026; EGF_3; 6.
PROSITE; PS01187; EGF_CA; 2.
EGF-like domain.
SEQUENCE 642 AA; 70655 MW; 56AFB4013E1C2AE2 CRC64;

Query Match 46.8%; Score 1945; DB 2; Length 642;
Best Local Similarity 47.7%; Pred. No. 3.2e-121;
Matches 345; Conservative 107; Mismatches 185; Indels 86; Gaps 13;

QY 7 LTLALLSALLCRQVDSGVFELKLOEFVNKGLLSNRNCRGGPGAGGQOQDCITFF 66
DB 5 LLEVYAATLCLPLVYPAGVFKLHSF-----STPRACAAGK-----SCNIF 49
QY 67 RVCLKHQASVPEPPCTYCSAITPVLGANSFSPDGGAGGADPAFSPNIPFPF 126
DB 50 RVCLKHQASVPEPPCTYCSAITPVLGANSFSPDGGAGGADPAFSPNIPFPF 100
QY 127 FSLIIEALHTSDPDLTENPERLISRLATORHLAVGEWSQDLHSGRTDLKYSYRVC 186
```

Db	101	FSHIESWTTNBAEQ--STENPNLUSRLATRRRLSIGEDWSQDHLGQSELRYSHVSC	159
Qy	187	DEHYEGEGSVFCRPRDRDFGHFTCGERGEKVCNPGWKGYQCTEPICLPCDCDQHGFCDK	246
Db	160	DEHYIGSDSCDYCRPRDDNFHYTCDQGNRLCSGWMKGEYCAEPICLPCSSESHGFCEL	219
Qy	247	PGECKRCVWCQRYCDECIIRYPGCLHGTCCQPCWQCNQCBGGLFCNQDLYNCTHHKPKC	306
Db	220	PGECKRMWQBELDECLIRYPGQHQSGSQFWECIQEKGWGLFCNQDLYNCTNHQPCR	279
Qy	307	NGATCNTGQSYTCSRPGYTGSSCETIENECDANPCKNKGGCTDLNENSYCTCPPGFY	366
Db	280	NGASCINTGQSYSCSRAGFTGTNCEIDINECASNPKKNGSGNDLENDYECVCRPGFY	339
Qy	367	GKNCELSAMTCADGPCFNGGRCCTDNPDG-GYSCRCPLGYSGFNCCKIDYCSSSPCANGA	425
Db	340	GKNCDISAMTCBDCGFCNGGTCEIKSSSGVGVCRPFNYHGSNCKEKIDRCTNSPLCNG	399
Qy	426	QCVDLGNSYICCOAGFTGRHCDNDVDCASFPVCNGTCCQGVNDYSCTCPPYGNKNC	485
Db	400	QCLDMGRNVLCRPGFSGPRCLNIDDCASSPCANGGTCVDAVNSTCSCTLYCGKDC	459
Qy	486	STPVSRCEHPCHNGATCHERSNRYYVCEARGYGLNCQFLPLBPQGPVVDFTBKYTE	545
Db	460	TLRVADACSSKPKNGGTCTYFTGTVNVCQPTGFMGTSCFPAVRHDPPTPAHRADSSNTLT-	518
Qy	546	GQNSQFPWTAVCAGIILVLLGLGCAATVVCRLKVOKRHQPEACRSETETMNNLANCQ	605
Db	519	-----MVCLG--LITFFLLGCGFVW--MRGMRGH-----	546
Qy	606	REKDISIVIGATQIKNTNKKYVDFHSDNSDKNGYKVRPSVDYNLVHLEKNEDSVKEEHG	665
Db	547	-----FNEKGRVNDLEPKNNLIEKEPH-----FKMFPNDPYLREKSS	583
Qy	666	KCAKETYDSABEKSQVLKSSDTSRRKRPDSVYSTSKDTKYQSVYVISEKDCICITA	725
Db	584	SKQKLQGSSEB-EENSGRRTORPKDPTKQCPTSRY--PEDGAVHPYIIL-PEPQCIFA	639
Qy	726	TEV 728	
Db	640	TEV 642	

Search completed: November 29, 2004, 13:26:03
Job time : 94.6462 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	4007	97.2	722	2	AAW11720	AAw11720	M-Delta-1
2	4003	97.1	722	6	ABU55873	ABu55873	Mouse not
3	4003	97.1	722	6	AAE34029	AAe34029	Murine no
4	3955	96.0	722	3	AAV79028	AAv79028	Murine de
5	3659.5	88.8	723	2	AAW18353	AAw18353	Prolifera
6	3659.5	88.8	723	2	AAW75492	AAw75492	Human del
7	3659.5	88.8	723	2	AAW94498	AAw94498	Human del
8	3659.5	88.8	723	3	AAV83227	AAv83227	PRO172 Po
9	3659.5	88.8	723	3	AAAB33422	AAb33422	Human PRO
10	3659.5	88.8	723	3	AAAB24388	AAb24388	Human PRO
11	3659.5	88.8	723	3	AAAB00172	AAb00172	PRO172 po
12	3659.5	88.8	723	4	AAU12344	AAu12344	Human PRO
13	3659.5	88.8	723	4	AAAB53064	AAb53064	Human ang
14	3659.5	88.8	723	6	ABO17788	ABo17788	Novel hum
15	3659.5	88.8	723	6	ABU81042	ABu81042	Human PRO
16	3659.5	88.8	723	6	ABU66742	ABu66742	Human PRO
17	3659.5	88.8	723	6	ABU59823	ABu59823	Novel sec
18	3659.5	88.8	723	6	ABO25013	ABo25013	Human sec
19	3659.5	88.8	723	6	ABU67018	ABu67018	Human sec
20	3659.5	88.8	723	6	ADA45865	Ada45865	Novel hum
21	3659.5	88.8	723	6	ADA76296	Ada76296	Human PRO
22	3659.5	88.8	723	6	ADA18946	Ada18946	Human PRO
23	3659.5	88.8	723	6	ADA61569	Ada61569	Homo sapi
24	3659.5	88.8	723	6	ADB19354	ADB19354	Novel hum
25	3659.5	88.8	723	6	ADB27895	ADB27895	Human PRO

Query Match	97.2%; Score 4007; DB 2; Length 722;	
Best Local Similarity	97.4%; Pred. No. 2.2e-225;	
Matches 703; Conservative	3; Mismatches 16; Indels 0; Gaps 0;	
QY 1	MGRSALALAVVALLCQWSSGVPELKLQBFVNNKGLLGNRNCRCGSGPPCACRTFFR 60	XX
DB 1	MGRSALALAVVALLCQWSSGVPELKLQBFVNNKGLLGNRNCRCGSGPPCACRTFFR 60	XX
QY 61	VLCKHYQASVPEPCTTGYSAVTPVLGVDLSPLDAGIDPAFNSNPFRFPFGFTWPCFTFS 120	XX
DB 61	VLCKHYQASVPEPCTTGYSAVTPVLGVDLSPLDAGIDPAFNSNPFRFPFGFTWPCFTFS 120	XX
QY 121	LIIEALHTDSPDLATENPERLISRLTTQRHLTVGEESQDLHSSGRDRLRYRFFVCDE 180	XX
DB 121	LIIEALHTDSPDLATENPERLISRLTTQRHLTVGEESQDLHSSGRDRLRYRFFVCDE 180	XX
QY 181	HYEGECVFCPRDADFHFCTGDRGKMDPQWKGQYCTDPTCLPGCDQHGCKPKG 240	XX
DB 181	HYEGECVFCPRDADFHFCTGDRGKMDPQWKGQYCTDPTCLPGCDQHGCKPKG 240	XX
QY 241	ECKCRVQWGRYCDRCIRYBGCVTGCTCOQWQCNCEQWGLFCNQDLNCTHHKPCRN 300	XX
DB 241	ECKCRVQWGRYCDRCIRYBGCVTGCTCOQWQCNCEQWGLFCNQDLNCTHHKPCRN 300	XX
QY 301	ATCTNTGQSGYTCSCRPYGTGANCELEVEDCAPSPCKNGASCCTDLEDSFCTCPPGFYK 360	XX
DB 301	ATCTNTGQSGYTCSCRPYGTGANCELEVEDCAPSPCKNGASCCTDLEDSFCTCPPGFYK 360	XX
QY 361	VCESAMTCADGFCNFGRCSDNPDPGYTCHCPLGFGNCEKKMDLCSGSSPCSNCAKV 420	XX
DB 361	VCESAMTCADGFCNFGRCSDNPDPGYTCHCPLGFGNCEKKMDLCSGSSPCSNCAKV 420	XX
QY 421	DLGNSVLCRCQAGSRYCEDNVDCCASPCANGTCTCRSDVDFSCCTCPGYTGKNCAP 480	XX
DB 421	DLGNSVLCRCQAGSRYCEDNVDCCASPCANGTCTCRSDVDFSCCTCPGYTGKNCAP 480	XX
QY 481	VSRCEHAPCHNGATCHQGRQYMCACQYGGPNCQFLLPEPPPGPMVVDLSERHMSQ 540	XX
DB 481	VSRCEHAPCHNGATCHQGRQYMCACQYGGPNCQFLLPEPPPGPMVVDLSERHMSQ 540	XX
QY 541	GPPFWAVCAGVVLVLLLLGCAAVVVCRLKLQKHQPPPCGGETTNNLANCQREK 600	XX
DB 541	GPPFWAVCAGVVLVLLLLGCAAVVVCRLKLQKHQPPPCGGETTNNLANCQREK 600	XX
QY 601	DVSVSIIGATQIKNTNKKADFHGDHGAESFKYRPTVDYVNLVRLDKGDEATVRDTHSK 660	XX
DB 601	DVSVSIIGATQIKNTNKKADFHGDHGAESFKYRPTVDYVNLVRLDKGDEATVRDTHSK 660	XX
QY 661	RTDKQSQSLQBRKSPQHLGVGRELNTENRPESVYTSKDTKYQSVVVLGAEDKCVIAT 720	XX
DB 661	RTDKQSQSLQBRKSPQHLGVGRELNTENRPESVYTSKDTKYQSVVVLGAEDKCVIAT 720	XX
QY 721	EV 722	XX
DB 721	EV 722	XX
RESULT 2		
ID	ABU55873	
XX	ABU55873 standard; protein; 722 AA.	
AC		
AC	ABU55873;	
XX		
XX	25-MAR-2003 (first entry)	
DT		
DE	Mouse notch ligand delta-like 1 protein.	
XX		
KW	Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation;	
KW	ligand; Parkinson's disease; Huntington's disease; motor neuron disease;	
KW	heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS;	
KW	acquired immunodeficiency syndrome.	
XX		


```
Qy 1 MGRSALALAVSALLCQWSSGVFELKQBFVNKGLGNRNCRCGSGPPCACRTFFR 60
Db 1 MGRSALALAVSALLCQWSSGVFELKQBFVNKGLGNRNCRCGSGPPCACRTFFR 60
Qy 61 VCLKHYQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNPFRPFPGFTWPGTFS 120
Db 61 VCLKHYQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNPFRPFPGFTWPGTFS 120
Qy 121 LIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSQDLHSSGRTDLRSYRFVUDE 180
Db 121 LIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSQDLHSSGRTDLRSYRFVUDE 180
Qy 181 HYEGGCVFRCRPRDDAFGHFTCGDRGEMKCDPWKGQYCTDPICLPGCDQHGKPCNG 240
Db 181 HYEGGCVFRCRPRDDAFGHFTCGDRGEMKCDPWKGQYCTDPICLPGCDQHGKPCNG 240
Qy 241 ECKCRVGMQGRYDECIRYPCVHGTCTQOPWQCNQCGWGLFCNQDLNYTHHKPCNG 300
Db 241 ECKCRVGMQGRYDECIRYPCVHGTCTQOPWQCNQCGWGLFCNQDLNYTHHKPCNG 300
Qy 301 ATCTNTQGSYTCSCRPGYTGANCELEVDCAFPCKNGASCTDLEDSFSCCTCPGFGYK 360
Db 301 ATCTNTQGSYTCSCRPGYTGANCELEVDCAFPCKNGASCTDLEDSFSCCTCPGFGYK 360
Qy 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKKMDLGGSSPSCNGAKCV 420
Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKKMDLGGSSPSCNGAKCV 420
Qy 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPCTCPGTYGKNCAP 480
Db 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPCTCPGTYGKNCAP 480
Qy 481 VSRCEHAPCHNGATCHORGORMYCECAGYGGPNCQFLLPEPPGPMVVDLSERHMSQ 540
Db 481 VSRCEHAPCHNGATCHORGORMYCECAGYGGPNCQFLLPEPPGPMVVDLSERHMSQ 540
Qy 541 GPPFWAVAGVLLVLLLLGCAAVVVCVRLKQHQPPPEPCGGTETETMNNLANCQREK 600
Db 541 GPPFWAVAGVLLVLLLLGCAAVVVCVRLKQHQPPPEPCGGTETETMNNLANCQREK 600
Qy 601 DVSYSIIIGATQIKNTNKKADPHGDHGAESKFVRYPTVDYVNLVRDLKGBEATVRDTHSK 660
Db 601 DVSYSIIIGATQIKNTNKKADPHGDHGAESKFVRYPTVDYVNLVRDLKGBEATVRDTHSK 660
Qy 661 RDTKCSQSLEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVIAT 720
Db 661 RDTKCSQSLEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVIAT 720
Qy 721 EV 722
Db 721 EV 722

RESULT 3
AAE34029
ID AAE34029 standard; protein; 722 AA.
XX
AC AAE34029;
XX
DT 02-MAY-2003 (first entry)
XX
XX Murine notch ligand delta-like 1 protein.
XX
XX Murine; drug screening; toxicology assay; signalling pathway;
XX
XX notch ligand delta-like 1.
XX
XX Mus sp.
XX
XX WO200290992-A2.
XX
XX 14-NOV-2002.
XX
```

```
PF 29-APR-2002; 2002WO-GB001946.
XX
PR 04-MAY-2001; 2001GB-00011004.
XX
PA (AXOR-) AXORDIA LTD.
XX
PI Andrews P, Draper J, Walsh J;
XX
XX WPI; 2003-120579/11.
XX
DR N-PSDB; AAD52523.
XX
XX
XX Identifying biologically active agents comprises cloning transfected
PT cells into a cell array, exposing the array to an agent to be tested, and
PT detecting signals generated by a reporter molecule as a result of
PT exposure to the agent.
XX
XX Claim 16; Fig 2; 90pp; English.
XX
XX The present invention relates to a novel screening method which enables
CC the identification of biologically active agents which mediate their
CC effect through the activation of genes. The method involves providing a
CC population of cells stably transfected with a nucleic acid encoding a
CC reporter molecule, cloning the transfected cells into a cell array,
CC exposing the array to at least one agent to be tested and detecting a
CC signal generated by the reporter molecule as a result of exposure to the
CC agent. The method is useful in identifying biologically active agents and
CC the genes through which the agents act, in screening potential drugs for
CC their ability to activate certain drug targets in a high-throughput
CC assay in identifying relationships between signalling pathways and
CC specific signals that could be useful in eventually directing the
CC differentiation of embryonic stem cells and in toxicology assays by
CC testing for unwanted activation or inhibition of specific signalling
CC pathways. The present sequence is murine notch ligand delta-like 1
CC protein used to illustrate the method of the invention
XX
XX Sequence 722 AA;
```

```
Query Match 97.1%; Score 4003; DB 6; Length 722;
Best Local Similarity 97.2%; Pred. No. 3.7e-225;
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
Qy 1 MGRSALALAVSALLCQWSSGVFELKQBFVNKGLGNRNCRCGSGPPCACRTFFR 60
Db 1 MGRSALALAVSALLCQWSSGVFELKQBFVNKGLGNRNCRCGSGPPCACRTFFR 60
Qy 61 VCLKHYQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNPFRPFPGFTWPGTFS 120
Db 61 VCLKHYQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNPFRPFPGFTWPGTFS 120
Qy 121 LIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSQDLHSSGRTDLRSYRFVUDE 180
Db 121 LIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSQDLHSSGRTDLRSYRFVUDE 180
Qy 181 HYEGGCVFRCRPRDDAFGHFTCGDRGEMKCDPWKGQYCTDPICLPGCDQHGKPCNG 240
Db 181 HYEGGCVFRCRPRDDAFGHFTCGDRGEMKCDPWKGQYCTDPICLPGCDQHGKPCNG 240
Qy 241 ECKCRVGMQGRYDECIRYPCVHGTCTQOPWQCNQCGWGLFCNQDLNYTHHKPCNG 300
Db 241 ECKCRVGMQGRYDECIRYPCVHGTCTQOPWQCNQCGWGLFCNQDLNYTHHKPCNG 300
Qy 301 ATCTNTQGSYTCSCRPGYTGANCELEVDCAFPCKNGASCTDLEDSFSCCTCPGFGYK 360
Db 301 ATCTNTQGSYTCSCRPGYTGANCELEVDCAFPCKNGASCTDLEDSFSCCTCPGFGYK 360
Qy 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKKMDLGGSSPSCNGAKCV 420
Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKKMDLGGSSPSCNGAKCV 420
Qy 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPCTCPGTYGKNCAP 480
Db 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPCTCPGTYGKNCAP 480
```

QY 481 VSRCEHAPCHNGATCHQGRQYMCACQYGGPNCQFLLPBPPGPMVVDLSERHMSOG 540
DB |||||
QY 481 VSRCEHAPCHNGATCHQGRQYMCACQYGGPNCQFLLPBPPGPMVVDLSERHMSOG 540
DB |||||
QY 541 GFFPWAACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGTETMNNLANCQREK 600
DB |||||
QY 541 GFFPWAACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGTETMNNLANCQREK 600
DB |||||
QY 601 DVSVSIIIGATQIKNTNKKADFHGDHGAESPKVRYPTVDYVNLVRLDKGDEATVRDTHSK 660
DB |||||
QY 601 DVSVSIIIGATQIKNTNKKADFHGDHGAESPKVRYPTVDYVNLVRLDKGDEATVRDTHSK 660
DB |||||
QY 661 RDTKQSSQSSAGEEIKIAPTLRGGEIPDRKRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720
DB |||||
QY 721 EV 722
DB ||
QY 721 EV 722
DB ||
RESULT 4
AA79028
ID AA79028 standard; protein; 722 AA.
XX
AC AA79028;
XX
DT 06-JUN-2000 (first entry)
XX
DE Murine delta protein amino acid sequence.
XX
KW Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;
KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;
KW tissue regeneration; liver cirrhosis; keloid formation; baldness;
KW inner ear disorder; mouse.
XX
OS Mus sp.
XX
PN WO200002897-A2.
XX
PD 20-JAN-2000.
XX
PF 13-JUL-1999; 99WO-US015817.
XX
PR 13-JUL-1998; 98US-0092513P.
PR 19-OCT-1998; 98US-0104834P.
XX
PA (UYVA) UNIV VALE.
XX
PI Artavanis-Tsakonas S, Rand MD, Qi H;
XX
DR WPI; 2000-282852/24.
XX
PT New cleavage peptide, nucleic acids and antibodies useful for diagnosis,
PT prevention and treatment of cancer, disorders of central nervous system,
PT cirrhosis and psoriasis.
XX
PS Claim 1; Fig 3; 177pp; English.
XX
CC This sequence represents the murine delta protein amino acid sequence.
CC Delta is a topothymic protein that contains a sequence which is cleaved
CC by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz
CC results in two fragments, a soluble amino terminal fragment consisting
CC essentially of the extracellular domain, and a membrane bound fragment
CC consisting of the transmembrane domain and the intracellular domain. The
CC soluble fragment is able to bind to Notch. Delta plays a key role in
CC differentiation, and therefore detection and measurement of delta
CC activation is important in the study of differentiation. The invention
CC relates to the delta cleavage peptides (the active fragment), and to
CC methods for detecting and measuring delta activation. Delta cleavage
CC peptides, and chimeric proteins are useful for modulating the activity of
CC Notch, delta or kuz or at least one of the signalling pathways in a cell
CC or organism, expressing Notch. By contacting a cell with kuz protein or

CC nucleic acid or its antibody, the activity or levels of delta protein is
CC modulated and vice versa. A delta cleavage peptide or its derivative
CC capable of binding kuz protein is useful for treating or preventing a
CC disease or disorder associated with increased delta activity or
CC expression such as cervical, breast, colon or lung cancer, melanoma or
CC seminoma in humans. A recombinant cell comprising a delta peptide is
CC useful for treating or preventing central nervous system disorders. A
CC delta cleavage peptide is useful for the diagnosis of diseases or
CC disorders associated with increased levels of Notch-delta protein binding
CC activity comprising measuring the ability of delta cleavage peptides in a
CC sample to bind kuz protein. A complex of delta protein and kuz is useful
CC for diagnosing or screening for the presence of, or predisposition to
CC developing a disease or disorder associated with aberrant levels of the
CC complex, comprising measuring the level or functional activity of the
CC complex or RNA encoding delta or kuz in a sample. The delta cleavage
CC peptide is also useful for promoting tissue regeneration and repair, for
CC treating liver cirrhosis, keloid formation, psoriasis, baldness and
CC degenerative or traumatic disorders of the sensory epithelium of the
CC inner ear
XX
SQ Sequence 722 AA;
Query Match 96.0%; Score 3955; DB 3; Length 722;
Best Local Similarity 96.1%; Pred. No. 2.3e-222;
Matches 694; Conservative 6; Mismatches 22; Indels 0; Gaps 0;
QY 1 MGRSALALAVVSALLCQWSSGVFELKLOEFVNKKLLGNRNCRCGGSGPPCACKTFPR 60
DB |||||
QY 1 MGRSALALAVVSALLCQWSSGVFELKLOEFVNKKLLGNRNCRCGGSGPPCACKTFPR 60
DB |||||
QY 61 VCLKHQYASVSEPPCTYGSVTPVLGVDSFSLPGAGIDPAFSPNPIRPFPGTWPGTFS 120
DB |||||
QY 61 VCLKHQYASVSEPPCTYGSVTPVLGVDSFSLPGAGIDPAFSPNPIRPFPGTWPGTFS 120
DB |||||
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEMSQDLHSSGRTDLRYSYRFVDE 180
DB |||||
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEMSQDLHSSGRTDLRYSYRFVDE 180
DB |||||
QY 181 HYGEGCSVFCPRDDAFGHFTCGDRGEMKCPGKQYCTDPICLPGCDDOHGYCDKPG 240
DB |||||
QY 181 HYGEGCSVFCPRDDAFGHFTCGDRGEMKCPGKQYCTDPICLPGCDDOHGYCDKPG 240
DB |||||
QY 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPMQCNQCEGMGLFCNODLNYCTHHKCRNG 300
DB |||||
QY 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPMQCNQCEGMGLFCNODLNYCTHHKCRNG 300
DB |||||
QY 301 ATCTNTGQSYTSCRCRPGYTGANCELEVDCEAPSPCKMGASCTDLEDSFSTCTPPGFYK 360
DB |||||
QY 301 ATCTNTGQSYTSCRCRPGYTGANCELEVDCEAPSPCKMGASCTDLEDSFSTCTPPGFYK 360
DB |||||
QY 361 VCELSAMTCADGFCFNGGRCSNPDGGYTCHCPLGFGSFCNCKMDLCSGSSPCSNCAKCV 420
DB |||||
QY 361 VCELSAMTCADGFCFNGGRCSNPDGGYTCHCPLGFGSFCNCKMDLCSGSSPCSNCAKCV 420
DB |||||
QY 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCDRDSVNDVDFCTCPPGYTGKNCAP 480
DB |||||
QY 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCDRDSVNDVDFCTCPPGYTGKNCAP 480
DB |||||
QY 481 VSRCEHAPCHNGATCHQGRQYMCACQYGGPNCQFLLPBPPGPMVVDLSERHMSOG 540
DB |||||
QY 481 VSRCEHAPCHNGATCHQGRQYMCACQYGGPNCQFLLPBPPGPMVVDLSERHMSOG 540
DB |||||
QY 541 GFFPWAACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGTETMNNLANCQREK 600
DB |||||
QY 541 GFFPWAACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGTETMNNLANCQREK 600
DB |||||
QY 601 DVSVSIIIGATQIKNTNKKADFHGDHGAESPKVRYPTVDYVNLVRLDKGDEATVRDTHSK 660
DB |||||
QY 601 DVSVSIIIGATQIKNTNKKADFHGDHGAESPKVRYPTVDYVNLVRLDKGDEATVRDTHSK 660
DB |||||
QY 661 RDTKQSSQSSAGEEIKIAPTLRGGEIPDRKRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720
DB |||||
QY 661 RDTKQSSQSSAGEEIKIAPTLRGGEIPDRKRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720
DB |||||

```

Qy 721 EV 722
Db 721 EV 722

RESULT 5
AAW18353
ID AAW18353 standard; protein; 723 AA.
AC AAW18353;
XX
XX
XX 11-FEB-1998 (first entry)
XX
XX Proliferation and differentiation suppression polypeptide.
DE
DE Proliferation; differentiation; suppression; human; delta-1; serrate-1;
KW blood cell; neuron; leukaemia; malignant tumour; immunosuppression.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..221
FT Protein /label= Signal
FT Protein /label= Differentiation_suppression_protein
XX
XX WO9719172-A1.
XX
XX 29-MAY-1997.
XX
XX 15-NOV-1996; 96WO-JP003356.
XX
XX 17-NOV-1995; 95JP-00299611.
XX 30-NOV-1995; 95JP-00311811.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX
XX Sakano S, Itoh A;
XX
XX WPI; 1997-298110/27.
XX N-PSDB; AAT70174.
XX
XX Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress
XX proliferation and differentiation of undifferentiated human blood cells.
XX
XX Claim 15; Page 77-82; 114pp; Japanese.
XX
XX The present sequence represents a polypeptide which suppresses
XX proliferation and differentiation of undifferentiated cells such as
XX neurons and blood cells. The polypeptide may be used for the prevention
XX and control of disorders involving undifferentiated cells, such as
XX leukaemia and malignant tumours, and improvement of blood formation, e.g.
XX after immunosuppression
XX
XX Sequence 723 AA;

Query Match 88.88; Score 3659.5; DB 2; Length 723;
Best Local Similarity 87.08; Pred. No. 3.6e-205;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

Qy 1 MGRSALALAVSALLCQVNSGVFELKQBFVNKKGLGNRNCRCGSG-PPCACRTFF 59
Db 1 MGRSALALAVSALLCQVNSGVFELKQBFVNKKGLGNRNCRCGSGAGPPCACRTFF 60
Qy 60 RVCLKHYQASVSPPTCTYGSATVPVLGVDSFSLPDGAGIDPAFNPPIRPPFGFTWPGTF 119
Db 61 RVCLKHYQASVSPPTCTYGSATVPVLGVDSFSLPDGAGADSAFNPPIRPPFGFTWPGTF 120
Qy 120 SLIIEALHTDSPDGLATENPERLISRLTTORHLTVGEWSQDLHSSQRTDLRYSYRFVCD 179
Db 121 SLIIEALHTDSPDGLATENPERLISRLATQRHLTVGEWSQDLHSSQRTDLKYSYRFVCD 180

```

DR N-PSDB; AAX16817.
XX Vascular cell controlling agent comprises polypeptide - which is human
PT notch ligand and is used as drug.
XX
XX
PS Disclosure; Page 16-19; 21pp; Japanese.
XX
XX This sequence represents the human delta-1 protein, which is a ligand of
CC the human notch protein. The protein or fragments, especially AAW75493-
CC W75495, can be used as a drug to control vascular cells. The sequences
CC were isolated and the truncated fragments were generated using the
CC primers AAX16818-X16831
XX
XX
SQ Sequence 723 AA;

Query Match 88.8%; Score 3659.5; DB 2; Length 723;
Best Local Similarity 87.0%; Pred. No. 3.8e-205;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGSG-PPCACRTFF 59
Db 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGAGPPPCACRTFF 60

QY 60 RVCLKHQASVPEPPCTYGSATVPVLGVDVSLPDGAGIDPAFNSPIRFPFGFTWPGTF 119
Db 61 RVCLKHQASVPEPPCTYGSATVPVLGVDVSLPDGAGADSAFNSPIRFPFGFTWPGTF 120

QY 120 SLIIIEALHTSDPDDLATENPERLISRLTQRLTVGEEWSQDLHSSGRDRLYSYRFVCD 179
Db 121 SLIIIEALHTSDPDDLATENPERLISRLTQRLTVGEEWSQDLHSSGRDRLKYSYRFVCD 180

QY 180 EHYGEGCSVFCRPRDDAFGHFTCGDRGKWCDCPGKGOYCTDPTCLPCDDOHHGVCCKP 239
Db 181 EHYGEGCSVFCRPRDDAFGHFTCGDRGKVCNPGWKGPYCTEPICLPGCDEQHGCCKP 240

QY 240 GECKRVGHWGRYCDICIRPGCVHGTCCQWQCNCQEGWGLFCNQDLNYCTHHKPCRN 299
Db 241 GECKRVGHWGRYCDICIRPGCVHGTCCQWQCNCQEGWGLFCNQDLNYCTHHKPCRN 300

QY 300 GATCTNTGGSYTCSCRPYTGATCBLGIDECDDSPCKNGGSCDLENSYSCTCPGFGY 359
Db 301 GATCTNTGGSYTCSCRPYTGATCBLGIDECDDSPCKNGGSCDLENSYSCTCPGFGY 360

QY 360 KYCELSAMTCADGPCFNGRCSDNPDGTYTCHPLGFSFNCCKWDLGSSPCSNKAC 419
Db 361 KICELSAMTCADGPCFNGRCSDNPDGTYTCHPLGFSFNCCKWDLGSSPCSNKAC 420

QY 420 VDLGNSYLCRCQAGFSGRYCDNVDPCASSPCANGGTCRDVNDFSCTCPGTYGNCSA 479
Db 421 VDLGDAYLCRCQAGFSGRHCDNVDPCASSPCANGGTCRDVNDFSCTCPGTYGNCSA 480

QY 480 PVSRCHEAPCHNGATCQGRQRYMCACAGYGGPNCQFLLPBPMPVMDLSERHMSQ 539
Db 481 PVSRCHEAPCHNGATCQGRHRYVCACAGYGGPNCQFLLPBPMPVMDLTK-LEQG 539

QY 540 GGFPPMVAVCAGVLLVLLLGCAAVVVCRLKLOKHQPPPCGGETETMNNLANCORE 599
Db 540 GGFPPMVAVCAGVLLVLLLGCAAVVVCRLKLOKHQPPPCGGETETMNNLANCORE 599

QY 600 KDVSIIIGATQIKNTNKKADFGHGRGAKSFPKRYPTVDNVLVDLKGDEATVRDTHS 659
Db 600 KDVSIIIGATQIKNTNKKADFGHGRGAKSFPKRYPTVDNVLVDLKGDDTAVRDAHS 659

QY 660 KRDTKQSQ-SLQEKRSFOHLGVGRFLTENRPESVYTSKOTKYOSVYVLSAEKDECVI 718
Db 660 KRDTKQSQSGEEKGTPTTLRGGSASERKRPDSGCSKDTKYOSVYVLSAEKDECVI 719

QY 719 ATEV 722
Db 720 ATEV 723

AAW94498
ID AAW94498 standard; protein; 723 AA.
XX
AC AAW94498;
XX
DT 22-APR-1999 (first entry)
XX
XX Human delta-1 protein.
DE Human; delta-1; delta-2; differentiation inhibitor; proliferation;
XX Human; delta-1; delta-2; differentiation inhibitor; proliferation;
KW leukaemia; malignant tumour.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= signal
FT Protein 22..723
FT /label= Delta-1

XX WO9851799-A1.
PN
XX
PD 19-NOV-1998.
XX
XX 13-MAY-1998; 98WO-JP002104.
PP
XX
XX 14-MAY-1997; 97JP-00124064.
PR
XX
XX (ASAH) ASAH KASEI KOGYO KK.
PA
XX
XX Sakano S;
PI
XX
XX WPI; 1999-070120/06.
DR N-PSDB; AAX16300.
XX
XX Peptide inhibiting the differentiation of undifferentiated blood - used
PT for treatment of cancer and other disorders and the culture of human
PT cells in vitro.
XX
XX Example 1; Page 64-69; 86pp; Japanese.
PS
XX
XX The present invention describes full length and shortened human delta-2
CC proteins. Human delta-2 is a differentiation inhibitor which inhibits the
CC differentiation of undifferentiated cells (other than brain or muscle
CC cells), such as blood cells, and enhances the proliferation of
CC undifferentiated blood cells. Products of human delta-2 may be used for
CC the treatment of diseases such as leukaemia and malignant tumours. They
CC may also be used in the culture of human cells in vitro, e.g. for
CC production of supplies of undifferentiated blood cells. The present
CC sequence represents human delta-1, from an example of the present
CC invention
XX
SQ Sequence 723 AA;

Query Match 88.8%; Score 3659.5; DB 2; Length 723;
Best Local Similarity 87.0%; Pred. No. 3.8e-205;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGSG-PPCACRTFF 59
Db 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGAGPPPCACRTFF 60

QY 60 RVCLKHQASVPEPPCTYGSATVPVLGVDVSLPDGAGIDPAFNSPIRFPFGFTWPGTF 119
Db 61 RVCLKHQASVPEPPCTYGSATVPVLGVDVSLPDGAGADSAFNSPIRFPFGFTWPGTF 120

QY 120 SLIIIEALHTSDPDDLATENPERLISRLTQRLTVGEEWSQDLHSSGRDRLYSYRFVCD 179
Db 121 SLIIIEALHTSDPDDLATENPERLISRLTQRLTVGEEWSQDLHSSGRDRLKYSYRFVCD 180

QY 180 EHYGEGCSVFCRPRDDAFGHFTCGDRGKWCDCPGKGOYCTDPTCLPCDDOHHGVCCKP 239
Db 181 EHYGEGCSVFCRPRDDAFGHFTCGDRGKVCNPGWKGPYCTEPICLPGCDEQHGCCKP 240

FT /note= "Casein kinase II phosphorylation site"
FT 671..675
FT /note= "Casein kinase II phosphorylation site"
FT 676..682
FT /note= "N-myristoylation site"
FT 683..689
FT /note= "N-myristoylation site"
FT 695..701
FT /note= "N-myristoylation site"
FT 698..702
FT /note= "Casein kinase II phosphorylation site"
PN WO200021996-A2.
XX
XX
PD 20-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023089.
XX
PR 13-OCT-1998; 98US-0104080P.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI;
PI Yuan J;
XX
XX WPI; 2000-317943/27.
DR N-PSDB; AA293703.
XX
XX Composition for inhibiting neoplastic cell growth and treating cancers of
PT ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
PT PRO538, PRO172 or PRO182 polypeptide or their agonist.
XX
XX Claim 12; Fig 8; 122pp; English.
XX
XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
CC polypeptide or their agonists, mixed with a carrier is useful for
CC inhibiting neoplastic growth and treating tumors such as cancers of
CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
CC central nervous system, melanoma and leukaemia
XX
SQ Sequence 723 AA;

Query Match 88.8%; Score 3659.5; DB 3; Length 723;
Best Local Similarity 87.0%; Pred. No. 3.8e-205;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKGLGNRCRCGGSG-PPCACRTFF 59
DB 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKGLGNRCRCGGAGPPPCACRTFF 60

QY 60 RVCLKHQASVSEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFNPPIRPFPGFTWPGTF 119
DB 61 RVCLKHQASVSEPPCTYGSATVPVLGVDSFSLPDGAGADSAFNPPIRPFPGFTWPGTF 120

QY 120 SLIIIEALHTDSPDDLATENPERLISRLTQRLTVGEEWSQDLHSSGRDLDLVSYRFVCD 179
DB 121 SLIIIEALHTDSPDDLATENPERLISRLTQRLTVGEEWSQDLHSSGRDLDLKYSTRFVCD 180

QY 180 EHYHGECSVFCRPRDDAFGHFTCGDRGKMWCDPGWKQGYCTDPICLPGCDDQHGYCDKP 239
DB 181 EHYHGECSVFCRPRDDAFGHFTGGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240

QY 240 GECKRVHGQRYCDECIIRYPCGVHGTCCQPCQNCQBGWGLFCNQDLNYCTHHKPCRN 299
DB 241 GECKRVHGQRYCDECIIRYPCGVHGTCCQPCQNCQBGWGLFCNQDLNYCTHHKPCRN 300

QY 300 GATCTNTGGSYTCSCRCRGVTGANCELEVEDECAPSPCKNGASCTDLEDSEFSTCPCPGFYG 359
DB 301 GATCTNTGGSYTCSCRCRGVTGATBELGIDECOPSECKNGGSCDLDENSYCTCPCPGFYG 360

QY 360 KVCLSAMTCADGCPFCNGRCSDNPDGGYTHCHPLGFSGFNCEKMDLCSGSPCSNGAKC 419
DB 361 KICLSAMTCADGCPFCNGRCSDSPDGGYSCRCPVGSGFNCEKKIDYCSSSPCSNGAKC 420

QY 420 VDLGNSYLRCQAGFGSGRYCEDNVDDCASSPCANGTCRDSVNDPSCCTCPPGVTGKNCSA 479
DB 421 VDLGDAYILRCQAGFGSGRHCDNDVDDCASSPCANGTCRDSVNDPSCCTCPPGVTGKNCSA 480

QY 480 PVSRCHEAPCHNGATCHORGYMCECAQGYGPNQCQFLLPPEPPGPMVVDLSERHMESQ 539
DB 481 PVSRCHEAPCHNGATCHERGHRYVCECARGYGPNQCQFLLPPEPPGPAVVDLLEK-LEGQ 539

QY 540 GGPFPMWAVCAGVILVLLGLGCAAVVVCVRUKLOKHQPPPPCGGETMTMNLANCORE 599
DB 540 GGPFPMWAVCAGVILVLLGLGCAAVVVCVRUKLOKHQPPADPCRGETMTMNLANCORE 599

QY 600 KDVSYSIIIGATQIKNTNKKADPHGDHAEKSFVKRYPTVDYLVLDLKGDDATVDRDTHS 659
DB 600 KDVSYSIIIGATQIKNTNKKADPHGDHAEKSFVKRYPTVDYLVLDLKGDDATVDRDTHS 659

QY 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENPESVYSTSKDTKYQSVVVLSAEKDECVI 718
DB 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENPESVYSTSKDTKYQSVVVLSEKDECVI 719

QY 719 ATEV 722
DB 720 ATEV 723

RESULT 9
AAB33422
ID AAB33422 standard; protein; 723 AA.
AC AAB33422;
DT 29-JAN-2001 (first entry)
DE Human PRO172 protein UNQ146 SEQ ID NO:41.
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
XX dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; Gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.

XX Homo sapiens.
OS
XX WO200053758-A2.
PN
XX 14-SEP-2000.
PD
XX 02-MAR-2000; 2000WO-US005841.
PF
XX 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX (GETH) GENENTECH INC.
PA Aehkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58587.
XX
XX
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
XX Claim 33; Fig 18; 309pp; English.
XX
XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
XX Sequence 723 AA;
Query Match 88.8%; Score 3659.5; DB 3; Length 723;
Best Local Similarity 87.0%; Pred. No. 3.8e-205;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;
Qy 1 MGRSALALAVSALLQVWSSGVFELKLOEFVNNKGLGNRNCCRGSG-PPCACRTFF 59
Db 1 MGRSALALAVSALLQVWSSGVFELKLOEFVNNKGLGNRNCCRGSGPPCACRTFF 60
Qy 60 RVCLKHYQASVSPPEPCTYGSATVTPVLGVDSFSLPDGGADSAFNSNIRFPFGTWPGTF 119

Db 61 RVCLKHYQASVSPPEPCTYGSATVTPVLGVDSFSLPDGGADSAFNSNIRFPFGTWPGTF 120
Qy 120 SLIIETALHTSPDLDLATENPERLISRLTTOHRLTVGBEWSQDLHSSGRTDLRYSYRFVCD 179
Db 121 SLIIETALHTSPDLDLATENPERLISRLATQHLTVGBEWSQDLHSSGRTDLKYSYRFVCD 180
Qy 180 EHYYGEGCSVFCPRDDAFGHFTCGDRGEKMCDFGWKQYCTDPICLPGCDDQHGKDP 239
Db 181 EHYYGEGCSVFCPRDDAFGHFTCGDRGEKVCNPGWKGPYCTEPICLPGCDEQHGKDP 240
Qy 240 GECKCRVGMGRYCDCEIRYRGVCHGTCCQPMQCNCOEGWGLFCNODLNYCTHHKCRN 299
Db 241 GECKCRVGMGRYCDCEIRYPGCLHGTCCQPMQCNCOEGWGLFCNODLNYCTHHKPCN 300
Qy 300 GATCTNTGQGSYTCSCRPYTGANCELEVEDCAPSPCKNGASCTDLDSDSFCSTCPPPGYG 359
Db 301 GATCTNTGQGSYTCSCRPYTGATCELGIDECDSPPCKNGSGCTDLENSYSCSTCPPPGYG 360
Qy 360 KVCELSAMTCADGFCFNGGRCSNPDGGYTCCHPLGFSGNCEKMDLCCSSPSCSNGAKC 419
Db 361 KICELSAMTCADGFCFNGGRCSNPDGGYSCRCFVGYSGFNCEKKIDYCSSSPSCSNGAKC 420
Qy 420 VDLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCTCRDSVNDPSTCTPPGYTGKCSA 479
Db 421 VDLGDAYLRCQAGFSGRHCDNDVDDCASSPCANGGTCTCRDGVNDFSTCTPPGYTGRNCSA 480
Qy 480 PVSRCHEAPCHNGATCHORGYMCECAQGVGGNCOFLLPEPPPGPMVVDLSBRHMSQ 539
Db 481 PVSRCHEAPCHNGATCHERHRYVCECARGYGGNCOFLLPELPPGPAVDLTLTK-LEGQ 539
Qy 540 GGPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGTETMNNLANCORE 599
Db 540 GGPFPWVAVCAGVILVLLLLGCAAVVVCVRLRLQKHRRPADPCRGETETMNNLANCORE 599
Qy 600 KDVSYSIIIGATQIKNTNKKADFHGDHCAEKSFPKRYPTVDYNLVRLDKGEATVROTHS 659
Db 600 KDVSYSIIIGATQIKNTNKKADFHGDHCAEKSFPKRYPAVDYNLVQDLKGGDTAVRDAHS 659
Qy 660 KRDTKCSQ-SLOBKRSPQHLGVGRFLTENRSPESVYSTSKDTKYQSVYVLSAEKDECVI 718
Db 660 KRDTKCPQSSGSEKGTPTTLRGSEASERKRPDSGCGSTKDTKYQSVYVISEEKDECVI 719
Qy 719 ATEV 722
Db 720 ATEV 723
RESULT 10
AAB24388
ID AAB24388 standard; protein; 723 AA.
XX AAB24388;
AC AAB24388;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO172 protein sequence SEQ ID NO:4.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US028313.
XX
XX 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.

PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US0112252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PW, Wood WI;
XX
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77512.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
XX Claim 72; Fig 2; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 723 AA;

Query Match 88.8%; Score 3659.5; DB 3; Length 723;
Best Local Similarity 87.0%; Pred. No 3.8e-205;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRSALALAVSALCQWSSGVFELKIQEFVNKKGLGNRNCRRGGSG-PPCACRTFF 59
DB 1 MGRSALALAVSALCQWSSGVFELKIQEFVNKKGLGNRNCRRGGAGPPCACRTFF 60

QY 60 RVCLKHQASVSPPEPCTYGSATVPVLGVDSFSLPDGAGIDPAFSPNIRPFPGFTWPGTF 119
DB 61 RVCLKHQASVSPPEPCTYGSATVPVLGVDSFSLPDGAGIDPAFSPNIRPFPGFTWPGTF 120

QY 120 SLIIIEALHTDSPDLATENPERLISRLTQRLTVGEWSQDLHSSGRTDLRYSYRFVCD 179
DB 121 SLIIIEALHTDSPDLATENPERLISRLATQRLTVGEWSQDLHSSGRTDLKYSYRFVCD 180

QY 180 EHYVGGCSVFCRPRDADFCHFTCGDRGEMKCDPGWKQYCTDPICLPGCDQHGVCDP 239
DB 181 EHYVGGCSVFCRPRDADFCHFTCGDRGEMKCDPGWKQYCTDPICLPGCDQHGVCDP 240

QY 240 GECKRVGQGRYCDRCIRYPGCVHGTCCQWQCNCQEGWGLFCNQDLNYCTHHKPCRN 299
DB 241 GECKRVGQGRYCDRCIRYPGCVHGTCCQWQCNCQEGWGLFCNQDLNYCTHHKPCRN 300

QY 300 GATCTNTGGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSDSCTCPPGFYG 359

DB 301 GATCTNTGGSYTCSCRPGYTGATCELGIDECDPCKNGGCTDLENSYSCTCPGFGY 360
QY 360 KVCESAMTADGPGCFNGRCSDNDPGGYTHCHPLGFGFNCCKMDLGGSPSCNGAKC 419
DB 361 KVCESAMTADGPGCFNGRCSDSDPGGYSCRCPCVGYSGFNCCKIDYCSSSPSCNGAKC 420
QY 420 VDLGNSYLRCOAGSFGRYCEDNVDDCASSPCANGTCTCRDSVNDPSCCTCPGVTGNCSA 479
DB 421 VDLGDAYLRCOAGSFGRHCDNDVDDCASSPCANGTCTCRDGVNDFSCCTCPGVTGNCSA 480
QY 480 PVSRCHEHAPCHNGATCHORGYMCECAQGYGGPNCQFLPPEPPGPMVVDLSERHMSQ 539
DB 481 PVSRCHEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLPPEPPGPAVVDLLEK-LEGQ 539
QY 540 GGPPFWAVACAGVILVLLLLGCAAVVVCVRUKLOKHQPPPPCGGETMTNNLANCORE 599
DB 540 GGPPFWAVACAGVILVLLLLGCAAVVVCVRUKLOKHQPPPPCGGETMTNNLANCORE 599
QY 600 KDVSYSIIIGATQIKNTNKKADPHGDHGAESKSFVRYPTVDYNLVRDLKGDATVRDTHS 659
DB 600 KDVSYSIIIGATQIKNTNKKADPHGDHGAESKSFVRYPTVDYNLVRDLKGDATVRDTHS 659
QY 660 KRDTKCQSQ-SLQEKRRSPQHILGVGRFLTENRPESVYTSKDTKYQSVYVLSAEKDECVI 718
DB 660 KRDTKCQSQSGSBEKGTPTTLRGGEASERKEPDSGCTSKDTKYQSVYVLSAEKDECVI 719
QY 719 ATEV 722
DB 720 ATEV 723

RESULT 11
AAB00172
ID AAB00172 standard; protein; 723 AA.
AC AAB00172;
XX
XX 08-FEB-2001 (first entry)
DT PRO172 polypeptide.
DE
XX PRO211; PRO228; PRO338; PRO172; PRO182; neoplasia; inhibition; tumour;
KW treatment; therapy; agonist; antibody; breast cancer; ovarian cancer;
KW renal cancer; colorectal cancer; uterine cancer; prostate cancer;
KW lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder;
KW angiogenic disorder; immunologic disorder; human.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..21 /label= Signal peptide
FT Modified-site 2..8 /note= "N-myristoylation site"
FT Modified-site 37..43 /note= "N-myristoylation site"
FT Modified-site 40..46 /note= "N-myristoylation site"
FT Modified-site 93..97 /note= "N-myristoylation site"
FT Modified-site 98..104 /note= "Casein kinase II phosphorylation site"
FT Modified-site 99..105 /note= "N-myristoylation site"
FT Modified-site 131..135 /note= "N-myristoylation site"
FT Modified-site 154..158 /note= "Casein kinase II phosphorylation site"
FT Modified-site 176..185 /note= "Casein kinase II phosphorylation site"
FT Modified-site 203..207 /note= "Tyrosine kinase phosphorylation site"
FT Modified-site /note= "Casein kinase II phosphorylation site"

FT Domain 243..255 /label= EGF-like domain cysteine pattern signatur
FT Modified-site 252..261 /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 262..268 /note= "N-myristoylation site"
FT Domain 274..286 /label= EGF-like domain cysteine pattern signatur
FT Modified-site 281..287 /note= "N-myristoylation site"
FT Modified-site 282..288 /note= "N-myristoylation site"
FT Modified-site 301..307 /note= "N-myristoylation site"
FT Modified-site 310..316 /note= "N-myristoylation site"
FT Domain 314..326 /label= EGF-like domain cysteine pattern signatur
FT Modified-site 328..334 /note= "N-myristoylation site"
FT Modified-site 340..346 /note= "N-myristoylation site"
FT Modified-site 342..346 /note= "Casein kinase II phosphorylation site"
FT Modified-site 343..355 /note= "Asx hydroxylation site"
FT Modified-site 344..348 /note= "Casein kinase II phosphorylation site"
FT Domain 352..364 /note= "EGF-like domain cysteine pattern signatur"
FT Modified-site 369..373 /note= "Casein kinase II phosphorylation site"
FT Modified-site 378..384 /note= "N-myristoylation site"
FT Modified-site 387..393 /note= "N-myristoylation site"
FT Domain 391..403 /label= EGF-like domain cysteine pattern signatur
FT Modified-site 420..432 /note= "Asx hydroxylation site"
FT Domain 429..441 /label= EGF-like domain cysteine pattern signatur
FT Modified-site 457..461 /note= "Casein kinase II phosphorylation site"
FT Modified-site 458..480 /note= "Asx hydroxylation site"
FT Domain 467..479 /label= EGF-like domain cysteine pattern signatur
FT Modified-site 477..481 /note= "N-glycosylation site"
FT Modified-site 483..487 /note= "Casein kinase II phosphorylation site"
FT Modified-site 495..499 /note= "Casein kinase II phosphorylation site"
FT Domain 505..517 /label= EGF-like domain cysteine pattern signatur
FT Modified-site 512..518 /note= "N-myristoylation site"
FT Domain 548..568 /label= Transmembrane domain
FT Binding-site 552..563 /label= Prokaryotic membrane lipoprotein lipid a
FT Modified-site 659..663 /note= "Casein kinase II phosphorylation site"
FT Modified-site 660..664 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT Modified-site 670..674 /note= "Casein kinase II phosphorylation site"
FT Modified-site 671..675 /note= "Casein kinase phosphorylation site"
FT Modified-site 676..682 /note= "N-myristoylation site"

FT Modified-site 683..689 /note= "N-myristoylation site"
FT Modified-site 695..701 /note= "N-myristoylation site"
FT Modified-site 698..702 /note= "Casein kinase II phosphorylation site"
FT XX WO200055319-A1.
FN 21-SEP-2000.
XX 02-DEC-1999; 99WO-US028564.
XX 12-MAR-1999; 99US-0123957P.
XX 28-APR-1999; 99US-0131445P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 08-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 05-OCT-1999; 99WO-US023089.
XX 30-NOV-1999; 99WO-US028313.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
XX Yuan J;
XX WPI; 2000-638201/61.
XX N-PSDB; AAA54105.
XX PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for
XX treating tumors including cancers of the breast and lung, leukemia and
XX for identifying compounds capable of inhibiting growth of neoplastic
XX cells.
XX Claim 31; Fig 8; 133pp; English.
XX Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their
XX agonists (preferably anti-PRO agonist antibody or a small molecule
XX mimicking the biological activity of PRO polypeptide) are useful in vitro
XX or in vivo for inhibiting the growth of a tumour cell. Compositions
XX comprising the PRO polypeptides are useful for inhibiting neoplastic cell
XX growth and for treating cancer including breast, ovarian, renal,
XX colorectal, uterine, prostate, lung, bladder, central nervous system
XX cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also
XX useful for treating other disorders such as neuronal, glial, astrocytal,
XX hypothalamic and other glandular, macrophagal, epithelial, stromal,
XX blastocoealic disorders and inflammatory, angiogenic and immunologic
XX disorders as well as being useful for identifying agonists to PRO
XX polypeptides by contacting the polypeptide with a candidate molecule and
XX monitoring biological activity mediated by the polypeptide
XX Sequence 723 AA;
SQ Query Match 88.8%; Score 3659.5; DB 3; Length 723;
Best Local Similarity 87.0%; Pred. No. 3.8e-205;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;
Qy 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGSG-PPCACRTFF 59
Db 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGSGAGPPCACRTFF 60
Qy 60 RVCLKHQVQASVPEPCTYGSVTPVLGVDSFSLPDGAGIDPAFSPNIRPFPGTWPQTF 119
Db 61 RVCLKHQVQASVPEPCTYGSVTPVLGVDSFSLPDGAGIDPAFSPNIRPFPGTWPQTF 120
Qy 120 SLIIIEALHTDSPDDLATENPERLISRLTQRLHVTGSEWSQDLHSSGRTDLRSYRFVCD 179
Db 121 SLIIIEALHTDSPDDLATENPERLISRLTQRLHVTGSEWSQDLHSSGRTDLRSYRFVCD 180
Qy 180 EHYYGSCSVFCRPRDDAFGHFTCGRGEKVCNPGWKGPYCTBPICLPGCDQHGFCDKP 239
Db 181 EHYYGSCSVFCRPRDDAFGHFTCGRGEKVCNPGWKGPYCTBPICLPGCDQHGFCDKP 240

Db	1	MGRCALALAVLSALLQVWSSGVFELKLBQFVNKKGLLGNRNCRRGGAGPPPCACRTFF	60
Qy	60	RVCLKHYQASVSPPTCTYGSATVPVLGVDSFSLPDGAGIDPAFNSNPIRPFPGFTWCTF	119
Db	61	RVCLKHYQASVSPPTCTYGSATVPVLGVDSFSLPDGAGADSAFNSNPIRPFPGFTWCTF	120
Qy	120	SLIIETALHTDSDDLATENPERLLISRLTORHLTVGBEWSQDLHSSGRTDLRYSYRFVCD	179
Db	121	SLIIETALHTDSDDLATENPERLLISRLTORHLTVGBEWSQDLHSSGRTDLKYSYRFVCD	180
Qy	180	BHYHGECSVFCRRDDAFHGTCDGEGKWCDCGKQYCTDPTCLPGCDDQHGCDKP	239
Db	181	BHYHGECSVFCRRDDAFHGTCDGEGKWCDCGKQYCTDPTCLPGCDDQHGCDKP	240
Qy	240	GECKRQWQGRYDCECIYRPGCVHGTCCQWQNCQEGWGLFCNODLNYCTHHKPCRN	299
Db	241	GECKRQWQGRYDCECIYRPGCVHGTCCQWQNCQEGWGLFCNODLNYCTHHKPCRN	300
Qy	300	GATCTNTGQGYTCSRPGYTGANCELEVDCAFPSCKNGASCTDLEDSFCTCPPGFYG	359
Db	301	GATCTNTGQGYTCSRPGYTGANCELEVDCAFPSCKNGASCTDLEDSFCTCPPGFYG	360
Qy	360	KVCELSAMTCADGRCFNGRCSDNPDGTYCHPLGSGFNCCKMDLCSGSPCSNGAKC	419
Db	361	KVCELSAMTCADGRCFNGRCSDNPDGTYCHPLGSGFNCCKMDLCSGSPCSNGAKC	420
Qy	420	VDLGNLYLCRCQAGSGRGYCDNDVDDCASSPCANGGTCRDVNDPFCSTCPPGYTGKCSA	479
Db	421	VDLGNLYLCRCQAGSGRGYCDNDVDDCASSPCANGGTCRDVNDPFCSTCPPGYTGKCSA	480
Qy	480	PVSRCEHAPCHNGATCHQGRYMCCECAQYGGPNCQFLLPEPPPGMVVDLSRHMESQ	539
Db	481	PVSRCEHAPCHNGATCHQGRYMCCECAQYGGPNCQFLLPEPPPGMVVDLSRHMESQ	539
Qy	540	GGPPPMWAVACGVVLLVLLLLGCAAVVVCVRLKQKHQPPPCGGTETWNNLANCORE	599
Db	540	GGPPPMWAVACGVVLLVLLLLGCAAVVVCVRLKQKHQPPPCGGTETWNNLANCORE	599
Qy	600	KDVSIVSIIGATQIKNTNKKADPHGDHGAESKFVRVPTVDVNLVRLDKGEAVTRDHS	659
Db	600	KDVSIVSIIGATQIKNTNKKADPHGDHGAESKFVRVPTVDVNLVRLDKGEAVTRDHS	659
Qy	660	KRDTKCSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTKDTKYQSVYVLSAEKDCVI	718
Db	660	KRDTKCSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTKDTKYQSVYVLSAEKDCVI	719
Qy	719	ATEV 722	
Db	720	ATEV 723	
RESULT 13			
AAB53064			
Id	AAB53064 standard; protein; 723 AA..		
XX	AAB53064;		
XX	AAB53064;		
XX	28-FEB-2001 (first entry)		
XX	Human angiogenesis-associated protein PRO172, SEQ ID NO:2.		
XX	Human; angiogenesis-associated protein; PRO; endothelial cell growth;		
KW	cardiac hypertrophy; cardiovascular disorder; endothelial disorder;		
KW	angiogenic disorder; atherosclerosis; osteoporosis; hypertension;		
KW	myocardial infarction; diabetic retinopathy; rheumatoid arthritis;		
KW	Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;		
KW	Alzheimer's disease; Huntington's disease; stroke; drug screening;		
KW	gene therapy; transgenic animal.		
OS	Homo sapiens.		
XX	WO200053753-A2.		
PN			
XX			

PD	14-SEP-2000.	
XX		
PF	05-JAN-2000; 2000WO-US000219.	
XX		
PR	08-MAR-1999; 99WO-US005028.	
PR	12-MAR-1999; 99US-0123957P.	
PR	14-MAY-1999; 99US-0134287P.	
PR	02-JUN-1999; 99WO-US012252.	
PR	23-JUN-1999; 99US-0141037P.	
PR	20-JUL-1999; 99US-0144758P.	
PR	26-JUL-1999; 99US-0145698P.	
PR	01-SEP-1999; 99WO-US020111.	
PR	08-SEP-1999; 99WO-US020594.	
PR	15-SEP-1999; 99WO-US021090.	
PR	15-SEP-1999; 99WO-US021547.	
PR	05-OCT-1999; 99WO-US023089.	
PR	30-NOV-1999; 99WO-US028313.	
PR	30-NOV-1999; 99WO-US028409.	
PR	02-DEC-1999; 99WO-US028564.	
PR	02-DEC-1999; 99WO-US028565.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;	
PI	Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;	
PI	Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;	
XX		
DR	WPI; 2001-090793/10.	
DR	N-PSDB; AAC97368.	
XX		
PT	New isolated nucleic acid for producing a PRO polypeptide, analyzing	
PT	genetic disorders and treating cardiovascular, endothelial or angiogenic	
PT	disorders, such as atherosclerosis, wounds or cancer.	
XX		
PS	Claim 69; Fig 2; 293pp; English.	
XX		
CC	The invention relates to novel human angiogenesis-associated proteins	
CC	designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding	
CC	PRO proteins. The invention also relates to vectors and host cells	
CC	comprising a PRO nucleic acid, the recombinant production of a PRO	
CC	protein, PRO antibodies specific for a PRO protein, fusion proteins	
CC	comprising a PRO protein, agonists or antagonists of a PRO protein, and	
CC	compounds which inhibit the expression of a PRO gene. The invention	
CC	additionally encompasses methods of identifying modulators of PRO	
CC	expression or activity; diagnosing a cardiovascular, endothelial or	
CC	angiogenic disorder, or a susceptibility to such a disorder by detecting	
CC	mutations in a PRO gene, or the expression level of a PRO gene within a	
CC	particular tissue; treating a cardiovascular, endothelial or angiogenic	
CC	disorder via the administration of a PRO protein, PRO nucleic acid, or	
CC	PRO agonist or antagonist; a retroviral gene therapy vector comprising a	
CC	PRO nucleic acid; and methods of inhibiting or stimulating endothelial	
CC	cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the	
CC	administration of a PRO protein, or an agonist or antagonist thereof. PRO	
CC	nucleic acids, PRO proteins, antibodies against PRO proteins, PRO	
CC	agonists and PRO antagonists may be used as therapeutic agents to treat	
CC	cardiovascular, endothelial or angiogenic disorders, such as	
CC	atherosclerosis, osteoporosis, myocardial infarction, hypertension,	
CC	diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,	
CC	endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's	
CC	disease, or stroke. PRO nucleic acids are additionally useful in the	
CC	recombinant production of PRO proteins, as hybridisation probes to screen	
CC	libraries to isolate cDNAs with sequence identity to PRO proteins, to map	
CC	genes encoding PRO proteins, to analyse genetic disorders, and in gene	
CC	therapy. PRO nucleic acids can also be used to produce transgenic animals	
CC	useful for the development and screening of potential therapeutic agents.	
CC	The present sequence represents a PRO protein of the invention	
XX		
SQ	Sequence 723 AA;	
Query Match 88.8%; Score 3659.5; DB 4; Length 723;		
Best Local Similarity 87.0%; Pred. No. 3.8e-205;		
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;		

QY 1 MGRSALALAVSALLCQWSSGVFBLKLQEFVNNKGLGNRNCRCGSG-PPCACRTFF 59
Db 1 MGRSALALAVSALLCQWSSGVFBLKLQEFVNNKGLGNRNCRCGSGAGPPPCACRTFF 60
QY 60 RVCLKHQYQASVPEPCTTYSATVPVLGVDSFSLPDGAGIDPAFSPNIPFPFGFTWPGTF 119
Db 61 RVCLKHQYQASVPEPCTTYSATVPVLGVDSFSLPDGAGADSAFSPNIPFPFGFTWPGTF 120
QY 120 SLIIIEALHTSDDDLATENPERLISLTQORHLTVGEEWSQDLHSSGRTDLSYRFVCD 179
Db 121 SLIIIEALHTSDDDLATENPERLISLTATQORHLTVGEEWSQDLHSSGRTDLSYRFVCD 180
QY 180 EHYYGSGSVFCRPRDADFCHFTCGDRGEMKCDPGMKQYCTDPICLPGCDDQHGVCXDP 239
Db 181 EHYYGSGSVFCRPRDADFCHFTCGERGKVCNPGMKGYCTEPICLPGCDDQHGVCXDP 240
QY 240 GECKRVGQGRYDCIRIYPGCVHGTCCQPMQCNQCEGMGLFCNQDLNYCTHHKPCRN 299
Db 241 GECKRVGQGRYDCIRIYPGCLHGTCCQPMQCNQCEGMGLFCNQDLNYCTHHKPCRN 300
QY 300 GATCTNTGGSYTCSCRPYGTGANCELEVDENAPSPCKNGASCTDLEDSFCTCPRGFY 359
Db 301 GATCTNTGGSYTCSCRPYGTGATCLGIDECOPSPCKNGGSCDTLENSYSCTCPRGFY 360
QY 360 KVCESAMTCADGPCFNGRCSDNPDPGYTCHCPLGFGFNCCKMDLGGSPSCSNGAKC 419
Db 361 KVCESAMTCADGPCFNGRCSDSPDGGYSCRCPVGYSGFNCCKIDYCSSPSCSNGAKC 420
QY 420 VILGNSYLRCQAGFSGRYCEDNVDVDCASSPCANGGTCRDVNDFSCTCPRGYTGKNC 479
Db 421 VILGDAYLCRQAGFSGRHCDNVDVDCASSPCANGGTCRDVNDFSCTCPRGYTGKNC 480
QY 480 PVSRCHEAHCHGATCHQGRQYMCACQYGGPNCQFLLPBPQPMVVDLSERHMEQ 539
Db 481 PVSRCHEAHCHGATCHERGHRQYMCARGYGGPNCQFLLPBPQPMVVDLTER-LEG 539
QY 540 GGPFPWAVACAGVVLVLLLLGCAAVVVRKLQKHPQPPCGGETETMNNLANCQRE 599
Db 540 GGPFPWAVACAGVILVLLMLLCAAVVVRULRQKHPADPCRGETETMNNLANCQRE 599
QY 600 KQVSIIIGATQIKNTNKKADFHGDHGAESFKVRYPTVDNVLRLDGLKGBATVRDTHS 659
Db 600 KQVSIIIGATQIKNTNKKADFHGDHGAESKNGFKARYPAVDYVNLVQDLKGGDTAVRDAHS 659
QY 660 KBDTKCQSO-SLOEKERSQHLGVGFLENPEVSUYTSKTKYQSVVLSAEKDECVI 718
Db 660 KBDTKCQPGSGEKGTPPTLURGGEASERKRPDSCGTSKTKYQSVVVISEEKDECVI 719
QY 719 ATEV 722
Db 720 ATEV 723
RESULT 14
ID ABO17788
XX ABO17788 standard; protein; 723 AA.
AC ABO17788;
XX ABO17788;
XX 26-AUG-2003 (first entry)
DT Novel human secreted and transmembrane protein PRO172.
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.

XX Homo sapiens.
OS US2003032156-A1.
XX 13-FEB-2003.
PD 06-MAY-2002; 2002US-00140474.
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 09-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-341980/32.
 DR N-PSDB; ACD24025.

XX New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.

XX Claim 12; Fig 346; 660pp; English.

XX The invention describes an isolated nucleic acid (I) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (I) is used to
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
 CC the proliferation or differentiation of cells or gene expression,
 CC stimulate the release of proteoglycans, stimulate the release of cytokine
 CC from peripheral blood mononuclear cells, inhibit the release of A-peptide
 CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
 CC acid and polypeptide encoded by it, are useful for treating inflammatory
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, acquired immunodeficiency syndrome
 CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
 CC hybridisation probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
 CC This is the amino acid sequence of a novel human secreted and

CC transmembrane PRO polypeptide
 XX
 SQ Sequence 723 AA;
 Query Match 88.8%; Score 3659.5; DB 6; Length 723;
 Best Local Similarity 87.0%; Pred. No. 3.8e-205;
 Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;
 Qy 1 MGRSALALAVSALLCQVWSSGVFELKLOEFVNNKGLGNRRNCRGSG-PPCACRTFF 59
 Db 1 MGRSALALAVSALLCQVWSSGVFELKLOEFVNNKGLGNRRNCRGSGAGAGPPCACRTFF 60
 Qy 60 RVCLKHQVQASVSPPEPCTYGSVTPVLGVDSFSLPDGAGIDPAPSNIRPFPGTWTGTF 119
 Db 61 RVCLKHQVQASVSPPEPCTYGSVTPVLGVDSFSLPDGAGIDPAPSNIRPFPGTWTGTF 120
 Qy 120 SLIIIEALHTDSDPDLATENPERLISRLTTORHLTVGSEWSDLHSSGRTDLKYSYRVCD 179
 Db 121 SLIIIEALHTDSDPDLATENPERLISRLTTORHLTVGSEWSDLHSSGRTDLKYSYRVCD 180
 Qy 180 EHYVGECSVFCRPRDDAFGHFTCGDRGKXKCDPGWKGOYCTDPICLPGCDDORHYCDKP 239
 Db 181 EHYVGECSVFCRPRDDAFGHFTCGDRGKXKCDPGWKGOYCTDPICLPGCDDORHYCDKP 240
 Qy 240 GECKRVGMQGRYDCBCIRYPGCVHGTCCQPPWQCNQCEGWGLFCNQDLNYCTHHKPCRN 299
 Db 241 GECKRVGMQGRYDCBCIRYPGCVHGTCCQPPWQCNQCEGWGLFCNQDLNYCTHHKPCRN 300
 Qy 300 GATCTNTGQSGSYTCSRCRPGYTGANCELEVDCAEPSCKNGASCCTDLEDSFCTCPGFGY 359
 Db 301 GATCTNTGQSGSYTCSRCRPGYTGANCELEVDCAEPSCKNGASCCTDLEDSFCTCPGFGY 360
 Qy 360 KVCESAMTCAQDPCFNGGRCSNPDGGYTCCHPCLGFSGFNCEKMDLCSGSSPCSNKAKC 419
 Db 361 KVCESAMTCAQDPCFNGGRCSNPDGGYTCCHPCLGFSGFNCEKMDLCSGSSPCSNKAKC 420
 Qy 420 VDLGNSYLRCQAGFSGRYCEDNVDCASSPCANGGTCTCRDSVNDFSCCTPPGYTGKNCSA 479
 Db 421 VDLGDAYLCRCQAGFSGRHCDNVDCASSPCANGGTCTCRDSVNDFSCCTPPGYTGKNCSA 480
 Qy 480 PVSRCBAPCHNGATCCHQRCQRYMCECAQYGGPCNCOFLPEPPPGPMVVDLSERHMSQ 539
 Db 481 PVSRCBAPCHNGATCCHQRCQRYMCECAQYGGPCNCOFLPEPPPGPMVVDLSERHMSQ 539
 Qy 540 GGFPPWVAVCAGVVLVLLLLGCAA VVVCVRLKQHPPEPCGGTETMNNLANCORE 599
 Db 540 GGFPPWVAVCAGVVLVLLLLGCAA VVVCVRLKQHPPEPCGGTETMNNLANCORE 599
 Qy 600 KDVSYSIIIGATQIKNTNKKADPHGDHGAESKSPKRYPTVYDNLVRLDKGDEATVRDTHS 659
 Db 600 KDVSYSIIIGATQIKNTNKKADPHGDHGAESKSPKRYPTVYDNLVRLDKGDEATVRDTHS 659
 Qy 660 KRRTKQSO-SLOEKRSPOHLGVGRFLTENRRPESVYSTSKDTKYQSVYVLSAEKDCVI 718
 Db 660 KRRTKQSO-SLOEKRSPOHLGVGRFLTENRRPESVYSTSKDTKYQSVYVLSAEKDCVI 719
 Qy 719 ATEV 722
 Db 720 ATEV 723
 RESULT 15
 ID ABU81042 standard; protein; 723 AA.
 XX
 AC ABU81042;
 XX
 DT 23-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #173.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;

Query Match		88.8%;	Score 3659.5;	DB 6;	Length 723;
Best Local Similarity		87.0%;	Pred. No. 3.8e-205;		
Matches 630;		Conservative 46;	Mismatches 45;	Indels 3;	Gaps 3;
QY	1	MGRSALALAVSALLQVWSSGVFELKQBFVNNKGLLGNRNCRCGGSG-PPCACRTFF	59		
DB	1	MGRSALALAVLSALLQVWSSGVFELKQBFVNNKGLLGNRNCRCGGAGPPCACRTFF	60		
QY	60	RVCLKHYQASVSPEPCTYGSANTPVLGVDSFSLPDGAGIDPAFSPNIRPPFGFTWPGTF	119		
DB	61	RVCLKHYQASVSPEPCTYGSANTPVLGVDSFSLPDGAGDASAFSPNIRPPFGFTWPGTF	120		
QY	120	SLIIIEALHTDSDDLATENPERLISRLTTORHLTVGBEWSQDLHSSGRDLDLRSYRFVCD	179		
DB	121	SLIIIEALHTDSDDLATENPERLISRLATQRHLTVGBEWSQDLHSSGRDLDLKYSYRFVCD	180		
QY	180	EHYYGEGCSVFCRRDDAFGHFTCGDRGKMCDFGWKGQYCTDPICLPGCDDQHGDCDKP	239		
DB	181	EHYYGEGCSVFCRRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP	240		
QY	240	GECKCRVGMQGRYCDICIRYPCGVHGTCCQPWQCNCQEGWGLFCNODLNYCTHHKPCRN	299		
DB	241	GECKCRVGMQGRYCDICIRYPCGLHGTCCQPWQCNCQEGWGLFCNODLNYCTHHKPCKN	300		
QY	300	GATCTNTGQGSYTCSCRPGYTGANCELEVDDECAPSPCKNGASCCTDLEDSEFSCCTCPPGFGY	359		
DB	301	GATCTNTGQGSYTCSCRPGYTGATCELGIDECDFSPCKNGGSCDTLENSYSCTCPPGFGY	360		
QY	360	KVCELSAMTCADGCFNFGRCSDNPDDGGYTCHCPGLFSGFNCEKXMDLCSGSSPCSNAGKC	419		
DB	361	KICELSAMTCADGCFNFGRCSDSDPGGYSCRCFVYSGFNCEKKIDYCSSSPCSNAGKC	420		
QY	420	VDLGNSYLCRCQAGFSGRYCEDNVDCCASSPCANGGTCRDSVNDPFCCTCPGYTGKNCSA	479		
DB	421	VDLGDAYLCRCQAGFSGRHCDNVDCCASSPCANGGTCRDGVNDPFCCTCPGYTGRNCSA	480		
QY	480	PVSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLLPEPPGPMVVDLSERHMESQ	539		
DB	481	PVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVDLTK-LEGG	539		
QY	540	GGFPFWAVACGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGTETMNNLANCORE	599		
DB	540	GGFPFWAVACGVVLVLLLLGCAAVVVCVRLKLQKHPADPCRGETETMNNLANCORE	599		
QY	600	KDVSVSIIIGATQIKNTNKKADFHDGHAESKSPKRYPTVDYNLVRDLKGDEATVRDTHS	659		
DB	600	KDISVSIIIGATQIKNTNKKADFHDGHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS	659		
QY	660	KRDTKCQSQ-SLQKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI	718		
DB	660	KRDTKCQSQSSGEEKGTPTTLRGEASEERKRPDSCGCTSKDTKYQSVYVISEEKDECVI	719		
QY	719	ATEV 722			
DB	720	ATEV 723			

Search completed: November 29, 2004, 13:21:54
Job time : 77.9253 secs

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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:18:13 ; Search time 20.2231 Seconds
(without alignments)
2367.669 Million cell updates/sec

Title: US-09-783-931-12

Perfect score: 4121

Sequence: 1 MGRSALALAVSALLCQVW.....YQSVYVLSABKDECVATEV 722

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4121	100.0	722	3	US-08-981-392-12
2	4121	100.0	722	4	US-09-908-322-12
3	3971	96.4	720	3	US-08-872-855-4
4	3840.5	93.2	713	3	US-08-872-855-5
5	3659.5	88.8	723	3	US-09-068-740A-9
6	3659.5	88.8	723	4	US-09-423-753-27
7	3659.5	88.8	723	4	US-10-140-002-346
8	3631.5	88.1	723	4	US-09-641-612-6
9	3571.5	86.7	702	3	US-09-068-740A-4
10	3368	81.7	728	3	US-08-981-392-2
11	3368	81.7	728	4	US-09-908-322-2
12	3357.5	81.5	729	3	US-08-872-855-8
13	3167.5	76.9	721	4	US-08-981-392-5
14	3167.5	76.9	721	4	US-09-908-322-5
15	3161.5	76.7	721	3	US-08-872-855-7
16	2837	68.8	520	3	US-09-068-740A-3
17	2823.5	68.5	717	3	US-08-872-855-9
18	2462	59.7	578	4	US-08-981-392-13
19	2462	59.7	578	4	US-09-908-322-13
20	1885	45.7	642	3	US-08-872-855-10
21	1879.5	45.6	685	3	US-08-872-855-2
22	1879.5	45.6	685	4	US-09-423-753-25
23	1879.5	45.6	685	4	US-09-641-612-7
24	1879.5	45.6	685	4	US-10-140-002-88
25	1870	45.4	659	4	US-09-423-753-3
26	1654.5	40.1	500	4	US-09-423-753-2
27	1468.5	35.6	833	1	US-08-264-534-6

Sequence 2, Appli
Sequence 6, Appli
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Sequence 6, Appli
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Sequence 11, Appli
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Sequence 6, Appli
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Sequence 85, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 5, Appli
Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-981-392-12
; Sequence 12, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antier, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-392-12

Query Match 100.0%; Score 4121; DB 3; Length 722;
Best Local Similarity 100.0%; Pred. No. 1.7e-301;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGSGPPCACRTPFR 60
Db |||||
QY 1 MGRRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGSGPPCACRTPFR 60
Db |||||
QY 61 VCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
Db |||||
QY 61 VCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
Db |||||
QY 121 LIIEALHTSDPDLATENPERLISRLTTORHLTVGSEWSQDLHSSGRTDLRSYRFVCD 180
Db |||||
QY 121 LIIEALHTSDPDLATENPERLISRLTTORHLTVGSEWSQDLHSSGRTDLRSYRFVCD 180
Db |||||
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKCPG 240
Db |||||
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKCPG 240
Db |||||
QY 241 ECKCRVGMQGRYDCIRYPGCVHGTCCQPWQNCQEGWGLFCNQDLNYCTHHKPCRN 300
Db |||||
QY 241 ECKCRVGMQGRYDCIRYPGCVHGTCCQPWQNCQEGWGLFCNQDLNYCTHHKPCRN 300
Db |||||
QY 301 ATCTNTGQSGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTPPGFYK 360
Db |||||
QY 301 ATCTNTGQSGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTPPGFYK 360
Db |||||
QY 361 VCELSAMTCADGCFNGRCSDNPDGGYTCHCPLGFSGFNCKMDLCSGSSPCSNKACV 420
Db |||||
QY 361 VCELSAMTCADGCFNGRCSDNPDGGYTCHCPLGFSGFNCKMDLCSGSSPCSNKACV 420
Db |||||
QY 421 DLGNSYLRCQAGFSGRYCDNVDCCASSPCANGGTCRDSVNDFSCTCPGVTGKNC 480
Db |||||
QY 421 DLGNSYLRCQAGFSGRYCDNVDCCASSPCANGGTCRDSVNDFSCTCPGVTGKNC 480
Db |||||
QY 481 VSRCEHAPCHNGATQHQRQRYMCEACQYGGPNCOFLLEPPPPGMVVDLSERH 540
Db |||||
QY 481 VSRCEHAPCHNGATQHQRQRYMCEACQYGGPNCOFLLEPPPPGMVVDLSERH 540
Db |||||
QY 541 GPPFWAVACGVVLLVLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANC 600
Db |||||
QY 541 GPPFWAVACGVVLLVLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANC 600
Db |||||
QY 601 DVSVSIIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660
Db |||||
QY 601 DVSVSIIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660
Db |||||
QY 661 RDTKQOSQLQEKRRSPQHLGVGRFLTENRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720
Db |||||
QY 661 RDTKQOSQLQEKRRSPQHLGVGRFLTENRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720
Db |||||
QY 721 EV 722
Db |||||
QY 721 EV 722

RESULT 2
US-09-908-322-12
; Sequence 12, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-908-322-12
Query Match 100.0%; Score 4121; DB 4; Length 722;
Best Local Similarity 100.0%; Pred. No. 1.7e-301; Mismatches 0; Indels 0; Gaps 0;
Matches 722; Conservative 0;
QY 1 MGRRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGSGPPCACRTPFR 60
Db |||||
QY 1 MGRRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGSGPPCACRTPFR 60
Db |||||
QY 61 VCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
Db |||||
QY 61 VCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
Db |||||
QY 121 LIIEALHTSDPDLATENPERLISRLTTORHLTVGSEWSQDLHSSGRTDLRSYRFVCD 180
Db |||||
QY 121 LIIEALHTSDPDLATENPERLISRLTTORHLTVGSEWSQDLHSSGRTDLRSYRFVCD 180
Db |||||
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKCPG 240
Db |||||
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKCPG 240
Db |||||
QY 241 ECKCRVGMQGRYDCIRYPGCVHGTCCQPWQNCQEGWGLFCNQDLNYCTHHKPCRN 300
Db |||||
QY 241 ECKCRVGMQGRYDCIRYPGCVHGTCCQPWQNCQEGWGLFCNQDLNYCTHHKPCRN 300
Db |||||
QY 301 ATCTNTGQSGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTPPGFYK 360
Db |||||
QY 301 ATCTNTGQSGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTPPGFYK 360
Db |||||
QY 361 VCELSAMTCADGCFNGRCSDNPDGGYTCHCPLGFSGFNCKMDLCSGSSPCSNKACV 420
Db |||||
QY 361 VCELSAMTCADGCFNGRCSDNPDGGYTCHCPLGFSGFNCKMDLCSGSSPCSNKACV 420
Db |||||
QY 421 DLGNSYLRCQAGFSGRYCDNVDCCASSPCANGGTCRDSVNDFSCTCPGVTGKNC 480
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QY 421 DLGNSYLRCQAGFSGRYCDNVDCCASSPCANGGTCRDSVNDFSCTCPGVTGKNC 480
Db |||||
QY 481 VSRCEHAPCHNGATQHQRQRYMCEACQYGGPNCOFLLEPPPPGMVVDLSERH 540
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QY 481 VSRCEHAPCHNGATQHQRQRYMCEACQYGGPNCOFLLEPPPPGMVVDLSERH 540
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QY 541 GPPFWAVACGVVLLVLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANC 600
Db |||||
QY 541 GPPFWAVACGVVLLVLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANC 600
Db |||||

Qy 601 DVSVIIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDDEATVRDTHSK 660
Db 601 DVSVIIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDDEATVRDTHSK 660
Qy 661 RDTKQSQSLQEKRSPOHLGVGRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVIAT 720
Db 661 RDTKQSQSLQEKRSPOHLGVGRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVIAT 720
Qy 721 EV 722
Db 721 EV 722
RESULT 3
US-08-872-855-4
; Sequence 4, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-872-855-4
Query Match 96.4%; Score 3971; DB 3; Length 720;
Best Local Similarity 97.0%; Pred. No. 3.1e-250;
Matches 700; Conservative 4; Mismatches 16; Indels 2; Gaps 2;
Qy 1 MGRSALALAVSALLCQVWSSGVFELKQEFVNNKGLLGNRNCCRGSGPPCACRTFFR 60
Db 1 MGRSALALAVSALLCQVWSSGVFELKQEFVNNKGLLGNRNCCRGSGPPCACRTFFR 60
Qy 61 VCLKHQASVSEPPCTYGSATVPLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS 120
Db 61 VCLKH-QASVSEPPCTYGSATVPLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS 119
Qy 121 LIIEALHTDSDDLATENPERLISRLTTQRLHTVGEESODLHSSGRTDLRYSYRFVCD 180
Db 120 LIIEALHTDSDDLATENPERLISRLTTQRLHTVGEESODLHSSGRTDLRYSYRFVCD 178
Qy 181 HYYGEGSVFCRPRDDAFGHFTCGDRGKMCDCPGWKGYCTDPICLPGCDQHGKCPG 240

Db 179 HYYGEGSVFCRPRDDAFGHFTCGDRGKMCDCPGWKGYCTDPICLPGCDQHGKCPG 238
Qy 241 ECKRCVGMQGRYDCDECIRYPCGVHGTCCQWQNCNCGMGLFCNQDLNLYCTHHKPCENG 300
Db 239 ECKRCVGMQGRYDCDECIRYPCGVHGTCCQWQNCNCGMGLFCNQDLNLYCTHHKPCENG 298
Qy 301 ATCTNTCGSYTSCRPYTGANCELEVDCAEPCPKNGASCTDLEDSFSCTCPGFGYK 360
Db 299 ATCTNTCGSYTSCRPYTGANCELEVDCAEPCPKNGASCTDLEDSFSCTCPGFGYK 358
Qy 361 VCELSAMTCADGPCFNGRCSDNDPDGGYTCHCPLGFSGFNCEKMDLCCGSSPCNGAKCV 420
Db 359 VCELSAMTCADGPCFNGRCSDNDPDGGYTCHCPLGFSGFNCEKMDLCCGSSPCNGAKCV 418
Qy 421 DLGNSYLCRCQAGFSGRYCSNDVDDCASSPCANGGTCTCRDSVNDPSCCTCPGYTCNCSAP 480
Db 419 DLGNSYLCRCQAGFSGRYCSNDVDDCASSPCANGGTCTCRDSVNDPSCCTCPGYTCNCSAP 478
Qy 481 VSRCEHAPCHNGATCHQGRQYMCCECAQYGGNQCQLLPEPPGPMVVDLSERHMSQ 540
Db 479 VSRCEHAPCHNGATCHQGRQYMCCECAQYGGNQCQLLPEPPGPMVVDLSERHMSQ 538
Qy 541 GPPFWAVACAGVVLVLLLLGCAAVVVCRLKQKQPPPEPCGGTETETMNNLANCOREK 600
Db 539 GPPFWAVACAGVVLVLLLLGCAAVVVCRLKQKQPPPEPCGGTETETMNNLANCOREK 598
Qy 601 DVSVIIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDDEATVRDTHSK 660
Db 599 DVSVIIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDDEATVRDTHSK 658
Qy 661 RDTKQSQSLQEKRSPOHLGVGRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVIAT 720
Db 659 RDTKQSQSSAGEBKIAPTLRGGEIPDRKPEVYSTSKDTKYQSVVYLSAEKDECVIAT 718
Qy 721 EV 722
Db 719 EV 720
RESULT 4
US-08-872-855-5
; Sequence 5, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-872-855-4

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 713 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-872-855-5

Query Match 93.2%; Score 3840.5; DB 3; Length 713;

Best Local Similarity 93.4%; Pred. No. 2e-280;

Matches 674; Conservative 11; Mismatches 28; Indels 9; Gaps 2;

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DB 1 MGRSALALAVVSALLCQWSSGVFELKQLQEFVNKKGLGNRCRGGSGPPCACTTFR 60

QY 61 VCLKHQVQASVSEPPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTF 120

DB 61 VCLKHQVQASVSEPPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTF 120

QY 121 LIIEALHTDS PDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180

DB 121 LIIEALHTDS PDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 179

QY 181 HYYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKGOYCTDPICLPGCDDQHGCDKPG 240

DB 180 HYYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKGOYCTDPICLPGCDDQHGCDKPG 239

QY 241 ECKCRVGMQGRYDCIRYPCGVHGTGQPCQWQCNQCEGMMGLFCNQDLNYCTHHKPCRN 300

DB 240 ECKCRVGMQGRYDCIRYPCGVHGTGQPCQWQCNQCEGMMGLFCNQDLNYCTHHKPCRN 299

QY 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTCPGFGYK 360

DB 300 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTCPGFGYK 359

QY 361 VCELSAMTADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKMDLCSGSPCSNGAKCV 420

DB 360 VCELSAMTADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKMDLCSGSPCSNGAKCV 419

QY 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGPGYTGKNC 480

DB 420 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGPGYTGKNC 479

QY 481 VSRCEHAPCHNGATCHQGRQYMCCEAQQYGGPNCQFLPPEPPGPMVVDLSERHMSQ 540

DB 480 VSRCEHAPCHNGATCHQGRQYMCCEAQQYGGPNCQFLPPEPPGPMVVDLSERHMSQ 531

QY 541 GPPFWAVACAGVVLVLLLLGCAAVVVRLLKLOKHOPPEBCGGTETMNNLANCQREK 600

DB 532 GPPFWAVACAGVVLVLLLLGCAAVVVRLLKLOKHOPPEBCGGTETMNNLANCQREK 591

QY 601 DVSVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYVNLVRLDKGDEATVRDTHSK 660

DB 592 DVSVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYVNLVRLDKGDEATVRDTHSK 651

QY 661 RDTKQSQSLQEKRRSPQHLGVGRFLTENRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720

DB 652 RDTKQSQSQSAGEBKSTSLRGVEPDRKRPSPSVYSTSKDTKYQSVYVLSAEKDECVIAT 711

QY 721 EV 722

DB 712 EV 713

RESULT 5

US-09-068-740A-9

; Sequence 9, Application US/09068740A

; Patent No. 6337387

; GENERAL INFORMATION:

; APPLICANT: SAKANO, SEIJI

; APPLICANT: ITOH, AKIRA

; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

; FILE REFERENCE: KP-8447

; CURRENT APPLICATION NUMBER: US/09/068,740A

; CURRENT FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: JP 7-299611

; PRIOR FILING DATE: 1995-11-17

; PRIOR APPLICATION NUMBER: JP 7-311811

; PRIOR FILING DATE: 1995-11-30

; PRIOR APPLICATION NUMBER: PCT/JP96/03356

; PRIOR FILING DATE: 1996-11-15

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 723

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-068-740A-9

Query Match 88.8%; Score 3659.5; DB 3; Length 723;

Best Local Similarity 87.0%; Pred. No. 8e-267;

Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRSALALAVVSALLCQWSSGVFELKQLQEFVNKKGLGNRCRGGSG-PPCAARTFF 59

DB 1 MGRSALALAVVSALLCQWSSGVFELKQLQEFVNKKGLGNRCRGGSG-PPCAARTFF 60

QY 60 RVCLKHQVQASVSEPPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTF 119

DB 61 RVCLKHQVQASVSEPPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTF 120

QY 120 SLIIIEALHTDS PDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 179

DB 121 SLIIIEALHTDS PDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180

QY 180 EHYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKGOYCTDPICLPGCDDQHGCDKXP 239

DB 181 EHYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKGOYCTDPICLPGCDDQHGCDKXP 240

QY 240 GECKCRVGMQGRYDCIRYPCGVHGTGQPCQWQCNQCEGMMGLFCNQDLNYCTHHKPCRN 299

DB 241 GECKCRVGMQGRYDCIRYPCGVHGTGQPCQWQCNQCEGMMGLFCNQDLNYCTHHKPCRN 300

QY 300 GATCTNTGQGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTCPGPGYK 359

DB 301 GATCTNTGQGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTCPGPGYK 360

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DB 421 VDLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGPGYTGKNC 480

QY 480 PVSRCHEAPCHNGATCHQGRQYMCCEAQQYGGPNCQFLPPEPPGPMVVDLSERHMSQ 539

DB 481 PVSRCHEAPCHNGATCHQGRQYMCCEAQQYGGPNCQFLPPEPPGPMVVDLSERHMSQ 539

QY 540 GPPFWAVACAGVVLVLLLLGCAAVVVRLLKLOKHOPPEBCGGTETMNNLANCQRE 599

DB 540 GPPFWAVACAGVVLVLLLLGCAAVVVRLLKLOKHOPPEBCGGTETMNNLANCQRE 599

QY 600 KDVSVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYVNLVRLDKGDEATVRDTHS 659

DB 600 KDVSVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYVNLVRLDKGDEATVRDTHS 659

QY 660 KRDTKQSQSLQEKRRSPQHLGVGRFLTENRPSVYSTSKDTKYQSVYVLSAEKDECVI 718

DB 660 KRDTKQSQSQSAGEBKSTSLRGVEPDRKRPSPSVYSTSKDTKYQSVYVLSAEKDECVI 719

QY 719 ATEV 722

DB 720 ATEV 723

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RESULT 6
US-09-423-753-27
; Sequence 27, Application US/09423753
; Patent No. 6664098
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; FILE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR
; FILE REFERENCE: KP-8693
; CURRENT APPLICATION NUMBER: US/09/423,753
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/JP98/02104
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 9/124064
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-753-27

Query Match      88.8%; Score 3659.5; DB 4; Length 723;
Best Local Similarity 87.0%; Pred. No. 8e-267;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY      1 MGRSALALAVVSALLCQVWSSGVFELKLOEFVNKKGLLGNRNCRCGGSG-PPCACRTFF 59
DB      1 MGRSALALAVLSALLCQVWSSGVFELKLOEFVNKKGLLGNRNCRCGGAGPPPCACRTFF 60
QY      60 RVCLKHQVQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNIRPPFGFTWPGTF 119
DB      61 RVCLKHQVQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNIRPPFGFTWPGTF 120
QY      120 SLIIIEALHTDSPDLATENPERLISRLTORHLLTVGEWSQDLHSSGRTDLRYSYRFVCD 179
DB      121 SLIIIEALHTDSPDLATENPERLISRLTORHLLTVGEWSQDLHSSGRTDLRYSYRFVCD 180
QY      180 EHYGEGCSVFCRPRDDAFGHFTCGDRGKXCMDCGMKGOYCTDPICLPGCDDHQYCDKP 239
DB      181 EHYGEGCSVFCRPRDDAFGHFTCGDRGKXCMDCGMKGOYCTDPICLPGCDDHQYCDKP 240
QY      360 KVCLSAMTADGCFNRCRSDNPDDGGYTCCHPLGSGFNCEKXMDLCSGSSPCSNAGK 419
DB      361 KICLSAMTADGCFNRCRSDNPDDGGYTCCHPLGSGFNCEKXMDLCSGSSPCSNAGK 420
QY      420 VDLGNSYLRCQAGFSGRYCEBNDVDCASPCANGTTCRDSVNDFTCTCPPGYTGKXCSA 479
DB      421 VDLGDAYLRCQAGFSGRHCDNDVDCASPCANGTTCRDSVNDFTCTCPPGYTGKXCSA 480
QY      480 PVSRCHEAPCHNGATCHQRGORYMCECAQYGGPNCFLLPEPPGPMVYDLSEHMHESQ 539
DB      481 PVSRCHEAPCHNGATCHRGHRYVCECARGYGGPNCFLLPELPPGPAVVDLTK-LEGG 539
QY      540 GGPFPWAVACGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETETMNNLANCORE 599
DB      540 GGPFPWAVACGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETETMNNLANCORE 599
QY      600 KDVSVSIIGATQIKNTNKKADFDHGDHGAESKFVRYPTVDYLVNLRDLKGEATVRDTHS 659
DB      600 KDISVSIIGATQIKNTNKKADFDHGDHGAESKFVRYPTVDYLVNLRDLKGEATVRDTHS 659
QY      660 KRDTKQSQ-SLOEKRKRSQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 719
DB      660 KRDTKQSQ-SLOEKRKRSQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 719

RESULT 7
US-10-140-002-346
; Sequence 346, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-140-002-346

Query Match      88.8%; Score 3659.5; DB 4; Length 723;
Best Local Similarity 87.0%; Pred. No. 8e-267;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY      1 MGRSALALAVVSALLCQVWSSGVFELKLOEFVNKKGLLGNRNCRCGGSG-PPCACRTFF 59
DB      1 MGRSALALAVLSALLCQVWSSGVFELKLOEFVNKKGLLGNRNCRCGGAGPPPCACRTFF 60
QY      60 RVCLKHQVQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNIRPPFGFTWPGTF 119
DB      61 RVCLKHQVQASVSPPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNIRPPFGFTWPGTF 120
QY      120 SLIIIEALHTDSPDLATENPERLISRLTORHLLTVGEWSQDLHSSGRTDLRYSYRFVCD 179
DB      121 SLIIIEALHTDSPDLATENPERLISRLTORHLLTVGEWSQDLHSSGRTDLRYSYRFVCD 180
QY      180 EHYGEGCSVFCRPRDDAFGHFTCGDRGKXCMDCGMKGOYCTDPICLPGCDDHQYCDKP 239
DB      181 EHYGEGCSVFCRPRDDAFGHFTCGDRGKXCMDCGMKGOYCTDPICLPGCDDHQYCDKP 240
QY      240 GECKRVGMQGRYCDRCIRYPCVGHGTCQPPWQCNCOBEGHGLFCNODLNYCTHHKPCRN 299
DB      241 GECKRVGMQGRYCDRCIRYPCVGHGTCQPPWQCNCOBEGHGLFCNODLNYCTHHKPCRN 300
QY      300 GATCTNTGQSGSYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLDSFSCCTCPPGFYG 359
DB      301 GATCTNTGQSGSYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLDSFSCCTCPPGFYG 360
QY      360 KVCLSAMTADGCFNRCRSDNPDDGGYTCCHPLGSGFNCEKXMDLCSGSSPCSNAGK 419
DB      360 KVCLSAMTADGCFNRCRSDNPDDGGYTCCHPLGSGFNCEKXMDLCSGSSPCSNAGK 419
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Db 361 KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCVGYSGFNCCKKIDYCSSSPCSNGAKC 420
Qy 420 VDLGNSYLRCRCQAGSFRVCEDNVDDCASSPCANGGTCTCRDSVNDFSCTCPGGYTGKNCSA 479
Db 421 VDLGDAYLRCRCQAGSFRHCDNDVDDCASSPCANGGTCTCRDGVNDFSCCTCPGGYTGKNCSA 480
Qy 480 PVSRCBHAFCNGATCCHQGRYMCCEAGYGGPNCQFLLPEPPGPMVVDLSERHMQ 539
Db 481 PVSRCBHAFCNGATCCHQGRYMCCEAGYGGPNCQFLLPELPDPAVVDLTK-LEGQ 539
Qy 540 GGPFFWVAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGGETETMNNLANCQRE 599
Db 540 GGPFFWVAVCAGVILVLLMLLGGCAAVVVCVRLKQKHQPPADPCRGCTETMNNLANCQRE 599
Qy 600 KDVSIIIGATQIKNTNKKADPHGDHGAESKSFVRYPTVDYVNLVRLDKGDEATVRDTHS 659
Db 600 KDISVSIIGATQIKNTNKKADPHGDHGAESKSFVRYPTVDYVNLVRLDKGDDTAVRDAHS 659
Qy 660 KRDTCQSO-SLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYOSVVVLSAEKDECVI 718
Db 660 KRDTCQPOGSGEKGTPPTLRGGEASERKRPDSCGTSKDTKYOSVVVISEEKDECVI 719
Qy 719 ATEV 722
Db 720 ATEV 723

RESULT 8
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USBS THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-6

Query Match 88.1%; Score 3631.5; DB 4; Length 723;
Best Local Similarity 86.5%; Pred. No. 1e-264;
Matches 626; Conservative 46; Mismatches 49; Indels 3; Gaps 3;

Qy 1 MGRSRALAVSALICQVWSSGVFELKLOEFVNKKGLGNRNCRCGGSG-PPCACRTFF 59
Db 1 MGRSRALAVSALICQVWSSGVFELKLOEFVNKKGLGNRNCRCGGAGPPCACRTFF 60
Qy 60 RVCLKHQYASVSEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTF 119
Db 61 RVCLKHQYASVSEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTF 120
Qy 120 SLIIIEALHTDSPDLATENPERLISLRTORHLTVGEEWSQDLHSSGRTDLKYSYRFVCD 179
Db 121 SLIIIEALHTDSPDLATENPERLISLRTORHLTVGEEWSQDLHSSGRTDLKYSYRFVCD 180
Qy 180 EHYVGGCSVFCPRDDAFGHFTCGRGEKWCDCPKHKGQYCTDPICLPGCDDOHGKCDKP 239
Db 181 EHYVGGCSVFCPRDDAFGHFTCGRGEKWCDCPKHKGQYCTDPICLPGCDDOHGKCDKP 240
Qy 240 GECKRVGWQGRYCDRCIRYPGCVHGTCCOOPWCNCEQWGGGLFCNQDLNYCTHHKPCRN 299
Db 241 GECKRVGWQGRYCDRCIRYPGCVHGTCCOOPWCNCEQWGGGLFCNQDLNYCTHHKPCRN 300
Qy 300 GATCTNTGGSYTCSCRPGYTGANCSLEVDCAAPSCKNGASCTDLEDSCCTCPGFGY 359
Db 301 GATCTNTGGSYTCSCRPGYTGATCBLGIDECDDSPCKNGGSCDLEDSCCTCPGFGY 360

Qy 360 KVCELSAMTCADGPCFNGGRCSDNDGGYTHCPLGFGFNCCKMDLCCGSPCSNGAKC 419
Db 361 KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCVGYSGFNCCKKIDYCSSSPCSNGAKC 420
Qy 420 VDLGNSYLRCRCQAGSFRVCEDNVDDCASSPCANGGTCTCRDSVNDFSCTCPGGYTGKNCSA 479
Db 421 VDLGDAYLRCRCQAGSFRHCDNDVDDCASSPCANGGTCTCRDGVNDFSCCTCPGGYTGKNCSA 480
Qy 480 PVSRCBHAFCNGATCCHQGRYMCCEAGYGGPNCQFLLPEPPGPMVVDLSERHMQ 539
Db 481 PVSRCBHAFCNGATCCHQGRYMCCEAGYGGPNCQFLLPELPDPAVVDLTK-LEGQ 539
Qy 540 GGPFFWVAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGGETETMNNLANCQRE 599
Db 540 GGPFFWVAVCAGVILVLLMLLGGCAAVVVCVRLKQKHQPPADPCRGCTETMNNLANCQRE 599
Qy 600 KDVSIIIGATQIKNTNKKADPHGDHGAESKSFVRYPTVDYVNLVRLDKGDEATVRDTHS 659
Db 600 KDISVSIIGATQIKNTNKKADPHGDHGAESKSFVRYPTVDYVNLVRLDKGDDTAVRDAHS 659
Qy 660 KRDTCQSO-SLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYOSVVVLSAEKDECVI 718
Db 660 KRDTCQPOGSGEKGTPPTLRGGEASERKRPDSCGTSKDTKYOSVVVISEEKDECVI 719
Qy 719 ATEV 722
Db 720 ATEV 723

RESULT 9
US-09-068-740A-4
; Sequence 4, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-068-740A-4

Query Match 86.7%; Score 3571.5; DB 3; Length 702;
Best Local Similarity 87.1%; Pred. No. 3.2e-260;
Matches 612; Conservative 45; Mismatches 43; Indels 3; Gaps 3;

Qy 22 SGVFELKLOEFVNKKGLGNRNCRCGGSG-PPCACRTFFRVCLKHQYASVSEPPCTYGS 80
Db 1 SGVFELKLOEFVNKKGLGNRNCRCGGAGPPPCACRTFFRVCLKHQYASVSEPPCTYGS 60
Qy 81 AVTPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFSLIIIEALHTDSPDLATENPE 140
Db 61 AVTPVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFSLIIIEALHTDSPDLATENPE 120
Qy 141 RLISRLTTORHLTVGEEWSQDLHSSGRTDLKYSYRFVCDDEHYVGGCSVFCPRDDAFGH 200
Db 121 RLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDDEHYVGGCSVFCPRDDAFGH 180
Qy 201 FTCGRGEKWCDCPKHKGQYCTDPICLPGCDDOHGKCDKPGECKRVGWQGRYCDRCIRYP 260
Db 181 FTCGRGEKWCDCPKHKGQYCTEPICLPGCDEQHGKCDKPGECKRVGWQGRYCDRCIRYP 240

261	Qy	GCVHGTCCOOPQCNCOCBGGGLFCNODLNYCTHHKPCRNNGATCTNTGGSYTCSCRPGYT	320
241	Db	GCLHGTCCOOPQCNCOCBGGGLFCNODLNYCTHHKPCRNNGATCTNTGGSYTCSCRPGYT	300
321	Qy	GANCELEYDECAPSPCKNGASCTDLEDSEFSCTCPPGFYGKVCELSAMTCADGFCFNGGRC	380
301	Db	GATCELGTIDECPSPCKNNGGSCDTLENSYSTCTPPGYGKICELSAMTCADGFCFNGGRC	360
381	Qy	SDNPDGGYTCHCPGLGFSFNCCKMDLCSGSPCSNGAKCVDLGNISVLCRCQAGFSRYCE	440
361	Db	SDSPDGGYSCHPCVGYSGFNCCKIIDIYCSSPSCNGAKCVDLDGDAYLDCQAGFSRCHD	420
441	Qy	DNVDDCASSPCANGTCDRDSVNDPESCTCPPGYTGKNCAPVSRCEBAPCHNGATCHQRQ	500
421	Db	DNVDDCASSPCANGTCDRDVNDPESCTCPPGYTGKNCAPVSRCEBAPCHNGATCHERGH	480
501	Qy	RYMCCEAQQYGGPNCQFLLPPPPPMPVVDLSERHMESQGGFPFVAVCAGVVLVLLLL	560
481	Db	RYVCECARGYGGPNCQFLLPELPGPAVVDLITEK-LEGQGGFPFVAVCAGVILVLMLLL	539
561	Qy	GCAAVVVCVRLUKQHPPPBPCCGETETMNLANCOREKDVSVSIIIGATQIKNTNKKAD	620
540	Db	GCAAVVVCVRLUKHRPPADPCRGTEETMNLANCOREKDITSVSIIGATQIKNTNKKAD	599
621	Qy	FHGDHGAEKSSFKVRYPTVVDYNLVRDLKGDEATVRDTHSKRDTKCSQ-SLQEKERSPOH	679
600	Db	FHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDHASKRDTKCPQSGSSEEGKGTPTT	659
680	Qy	LGVRGFITENRPESVYSTSKDTQSQSVVLSABKDECVIATEV	722
660	Db	LRGGEASERKRPDSCGTSKDTQSQSVYVISEEKDECVIATEV	702

RESULT 10

US-08-981-392--2
; Sequence 2, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

```
Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
;
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
;
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Miarock, S Leellie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;
; US-09-908-322-2
;
; Query Match 81.7%; Score 3368; DB 4; Length 728;
; Best Local Similarity 78.5%; Pred. No. 6.5e-245;
; Matches 574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;
;
; QY 1 MGRSALALAVVSALL--CQVWSSGVFELKQEFVNKKGILLNRNCCRGSGP-----P 52
; DB 1 MGRFLLTLALLSALLCRQVDGSGVFELKQEFVNKKGILLNRNCCRGG-GPGGAGQQ 59
;
; QY 53 CACRTFFRCLXHYQASVSPERCTYGSATPVLGVDSPSLDGA-GIDPAFSNPIRPF 111
; DB 60 CDCKTFFRCLXHYQASVSPERCTYGSATPVLGANSFSPVDGAGDAPAFSNPIRPF 119
;
; QY 112 GFTWPGTFSLLIETALHSDPDLATENPERLISRLTQRHLTVGEWSQDLHSSGRTDLR 171
; DB 120 GFTWPGTFSLLIETALHSDPDLATTENPERLISRLATQRLHVLAGEWSQDLHSSGRTDLK 179
;
; QY 172 YSYRFVCDHYHGGCVSFCRRPDDAFGHFTCGDRGKMCDPGWKQYCTDPICLPGCCD 231
; DB 180 YSYRFVCDHYHGGCVSFCRRPDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCCD 239
;
; QY 232 QHCYCDKPECKRCVWQGRYCDCEIRYPCVHGTQCPQCNQCGWGLFCNQDLNYC 291
; DB 240 QHGFCDKPECKRCVWQGRYCDCEIRYPCGLHGTQQPQCNQCGWGLFCNQDLNYC 299
;
; QY 292 THHKPCRNATCTNTQGSYTCSCRGYTGANCELEVDCECAPSKCNAGASCTDLEDSPSC 351
; DB 300 THHKPCRNATCTNTQGSYTCSCRGYTGSSCEIEINECDANPCNKGSCSTDLENSYSC 359
;
; QY 352 TCPPGYGVKVELSAMTCADGPFNGGRCSNDPDGYTCHPLGFGFNCCKMDLCGSS 411
; DB 360 TCPPGYGVKVELSAMTCADGPFNGGRCTDNDPDGYSRCPLGYSGFNCCKIDYCSSS 419
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412 PCSNGAKCVDLGNLSYLCRCQAGFSRGYCEBDNVDDCCASSPCANGGTCTCRDVSNDPSCCTCPPG 471
; 420 PCNAGACQVDLGNLSYLCRCQAGFTGRHCDNDVDDCASPCVNGGTCTQDGVNDYSCTCPPG 479
;
; QY 472 YTGKNCSPVSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLLPEPPPPGPMVVDL 531
; DB 480 YNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPQGPVVDV 539
;
; QY 532 SERHMSQGGPPPVAVAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGTETWN 591
; DB 540 TEKYTEGQNSQFPWIAVCAGIILVLLMLLGCAAVVVCVRLKVKQRHHQPEACRSETETWN 599
;
; QY 592 NLANCOREKDVSVSIIGATQIKNTNKKADFDHGDHGAEKSSFKVRYPTVDYNLVRDLKGD 651
; DB 600 NLANCOREKDISISVIGATQIKNTNKKVDHSDN-SDKNGYKVRYPVDYNLVHLEK-NE 657
;
; QY 652 ATVRDTHSKRDTKCSQSLQEKRRSPQHLGVGRFUTENRPESVYSTSKDTKYQSVVLSA 711
; DB 658 DSVKEHGKCEAKCTYDSEAEKSAVLKSSDTSERKRKPDVSVYSTSKDTKYQSVVVIS 717
;
; QY 712 EKDECVIATEV 722
; DB 718 EKDECIATEV 728
;
; RESULT 12
; US-08-872-855-8
; Sequence 8, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-872-855-8
;
; Query Match 81.5%; Score 3357.5; DB 3; Length 729;
; Best Local Similarity 78.4%; Pred. No. 4e-244;
; Matches 574; Conservative 73; Mismatches 72; Indels 13; Gaps 7;
;
; QY 1 MGRSALALAVVSALL--CQVWSSGVFELKQEFVNKKGILLNRNCCRGSGP-----P 52
; DB 1 MGRFLLTLALLSALLCRQVDGSGVFELKQEFVNKKGILLNRNCCRGG-GPGGAGQQ 59
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Db 1 MGRFLLTLALLSALLCRQVDGSGVFELKLOEFVNNKGLLNRRNCCRGG-GPGAGQQQ 59
Qy 53 CACRTFRVCLKHQASVSPPPCTYGSATVPLGVDSFSLPDGA-GIDPAFSPNIRPPF 111
Db 60 CDCRTFRVCLKHQASVSPPPCTYGSATVPLGVDSFSLPDGA-GIDPAFSPNIRPPF 119
Qy 112 GFTWPGTFSLLIEALHTDSDPLATENPERLISRLTORHLTVGEWSQDLHSSGRDLR 171
Db 120 GFTWPGTFSLLIEALHTDSDPLATENPERLISRLTORHLTVGEWSQDLHSSGRDLR 179
Qy 172 YSYRFVDEHYVGGCSVFCRPRDDAFGHFTCGDRGKMCDDPGWKGYCTDPICLPGCDD 231
Db 180 YSYRFVDEHYVGGCSVFCRPRDDAFGHFTCGDRGKMCDDPGWKGYCTDPICLPGCDD 239
Qy 232 QHGYCDKPGCEKCRVGMQGRYCDICIRYPCGVHGTCCQPMQCNCQEGWGLFCNQDLNYC 291
Db 240 QHGYCDKPGCEKCRVGMQGRYCDICIRYPCGVHGTCCQPMQCNCQEGWGLFCNQDLNYC 299
Qy 292 THHPKCRNGATCTNTGQSYTCRCPGYTGANCLEVDCEAPSPCKNGASCTDLEDSPSC 351
Db 300 THHPKCRNGATCTNTGQSYTCRCPGYTGANCLEVDCEAPSPCKNGASCTDLEDSPSC 359
Qy 352 TCPGFGYKVCESLMTCADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKNDLCSS 411
Db 360 TCPGFGYKVCESLMTCADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKNDLCSS 419
Qy 412 PCSNGAK-CVDLGNLSYLCRCQAGSGRYCEDNVDCCASSPCANGTCRDSVNDPSCCTPP 470
Db 420 PCANGAACVDLGNLSYLCRCQAGSGRYCEDNVDCCASSPCANGTCRDSVNDPSCCTPP 479
Qy 471 GYTGNKGSAPVSRCEHAPCHNGATCHORGYMCECAQGYGPNQCQLLPPPPGPMVVD 530
Db 480 GYNGKNGSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCQQLLPPPPGPMVVD 539
Qy 531 LSRHMSQSGPFPWAVCAVGLVALLLGCAGVAVVVCRLKQKHOPPPPCGGTETM 590
Db 540 FTEKTEGNSQFPWIAVCAVGLVALLLGCAGVAVVVCRLKQKHOPPPPCGGTETM 599
Qy 591 NNLANCOREKDVSVIIGATQIKNTNKKADPHGDHGAESFKYRYPTVDVNLVRLDGLD 650
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Db 658 EDSVKEEHGKCAKCTYDSEAEBSAVQLKSSDTSERKRPDSVYSTSKOTKYQSVYVLS 717
Qy 711 AEKDECIATVEV 722
Db 718 BEKDECIATVEV 729

RESULT 13

US-08-981-392-5

; Sequence 5, Application US/08981392

; Patent No. 6262025

; GENERAL INFORMATION:

; APPLICANT: Ish-Horowitz, David

; APPLICANT: Henrique, Domingos Manuel Pinto

; APPLICANT: Lewis, Julian Hart

; APPLICANT: Artavanis-Tsakonas, Spyridon

; APPLICANT: Gray, Grace

; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES

; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/981,392

; FILING DATE: 22-DEC-1997

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Antler, Adriane M.

; REGISTRATION NUMBER: 32,605

; REFERENCE/DOCKET NUMBER: 7326-038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-869-8864

; TELEEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 721 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-08-981-392-5

Query Match 76.9%; Score 3167.5; DB 3; Length 721;

Best Local Similarity 72.9%; Pred. No. 7.5e-230;

Matches 534; Conservative 89; Mismatches 87; Indels 23; Gaps 5;

Qy 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNNKGLLNRRNCCRGSGGPP---CACRT 57

Db 1 MGQRMULTLVLAVLAVLQISCSGLFELRLOEFVNNKGLLNRRNCCRGSLASLQRCCKT 60

Qy 58 FFRVCLKHQASVSPPPCTYGSATVPLGVDSFSLPDGAGIDPAFNPFRFPFGFTWPG 117

Db 61 FFRVCLKHQASVSPPPCTYGSATVPLGVDSFSLPDGAGIDPAFNPFRFPFGFTWPG 120

Qy 118 TFSLLIEALHTDSDPLATENPERLISRLTORHLTVGEWSQDLHSSGRDLYSYRNV 177

Db 121 TFSLLIEALHTDSDPLATENPERLISRLTORHLTVGEWSQDLHSSGRDLYSYRNV 180

Qy 178 CDEHYGEGSVCRPRDDAFGHFTCGDRGKMCDDPGWKGYCTDPICLPGCDDHGYCD 237

Db 181 CDEHYGEGSVCRPRDDAFGHFTCGDRGKMCDDPGWKGYCTDPICLPGCDDHGYCD 240

Qy 238 KPBECKCRVGMQGRYCDICIRYPCGVHGTCCQPMQCNCQEGWGLFCNQDLNYCTHKKPC 297

Db 241 KPBECKCRVGMQGRYCDICIRYPCGVHGTCCQPMQCNCQEGWGLFCNQDLNYCTHKKPC 300

Qy 298 RNGATCTNTGQSYTCRCPGYTGANCELEVDCEAPSPCKNGASCTDLEDSPSCPPGF 357

Db 301 RNGATCTNTGQSYTCRCPGYTGANCELEVDCEAPSPCKNGASCTDLEDSPSCPPGF 360

Qy 358 YGKVCESLMTCADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKNDLCSSGPCSNGA 417

Db 361 YGKVCESLMTCADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKNDLCSSGPCSNGA 420

Qy 418 KCVDLGNLSYLCRCQAGSGRYCEDNVDCCASSPCANGTCRDSVNDPSCCTPPYTGNC 477

Db 421 KCVDLGNLSYLCRCQAGSGRYCEDNVDCCASSPCANGTCRDSVNDPSCCTPPYTGNC 480

Qy 478 SAPVSRCEHAPCHNGATCHORGYMCECAQGYGPNQCQLLPPPPGPMVVDLSERHME 537

Db 481 SAPVSRCEHAPCHNGATCHORGYMCECAQGYGPNQCQLLPPPPGPMVVDLSERHME 538

Qy 538 SQGGPFPWAVCAVGLVALLLGCAGVAVVVCRLKQKHOPPPPCGGTETMNNLANCQ 597

Db 539 SQGGPFPWAVCAVGLVALLLGCAGVAVVVCRLKQKHOPPPPCGGTETMNNLANCQ 598

Qy 598 REKDVSVIIGATQIKNTNKKADPHGDHGAESFKYRYPTVDVNLVRLDGLDGEATVRDT 657

Db 599 REKDVSVIIGATQIKNTNKKADPHGDHGAESFKYRYPTVDVNLVRLDGLDGEATVRDT 657

Qy 658 HSKRDTKQCS-----QSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVL 709

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QY 710 SAEKDECIATEV 722
Db 709 SDEKDECIATEV 721

RESULT 14
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; Sequence 5, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Atavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5

Query Match 76.9%; Score 3167.5; DB 4; Length 721;
Best Local Similarity 72.9%; Pred. No. 7.5e-230;
Matches 534; Conservative 89; Mismatches 87; Indels 23; Gaps 5;

QY 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLGNRCRCGGSGPP---CACT 57
Db 1 MGQQRMLTLVLAVLCQISCSGLFELRLQEFVNKKGLGNMNCRCRPGSLASLQRCCKT 60
QY 58 FFRVCLKHQASVPEPCTYGSVAVPLVGVFSFSLPDGAGIDPAFNSNPIRPFPGFTWPG 117
Db 61 FFRICLKHQNSVPEPCTYGVAVPLVGVFSFVVPSSNADPTFNSNPIRPFPGFTWPG 120
QY 118 TFSLIIEALHTSDPDLATENPERLISRLTQRHLTVGSEWQDLHSSGRTDLRYSYRNV 177
Db 121 TFSLIIEALHADSDADLNTENPERLISRLATQRHLTVGSEWQDLHSSDRTTELKYSYRNV 180

QY 178 CDEHYVYGGCSVFCRPRDDAFGHFTCGDRGEKMCDPGMKGQYCTDPICLPGCCDDQHGCD 237
Db 181 CDEYVYGGCSYCRPRDDAFGHFSGEKGKLCNPMWKGLYCTEPICLPGCCDEHHGYCD 240
QY 238 KPECKCRVGMQGRYCDCEIRYPGCVHGTTCQOPWQCNQCEGWMGGLFCNODLNYCTHHKPC 237
Db 241 KPECKCRVGMQGRYCDCEIRYPGCLHGTTCQOPWQCNQCEGWMGGLFCNODLNYCTHHKPC 300
QY 298 RNGATCTNTGSGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLBDSFSCTCPPGF 357
Db 301 ENGATCTNTGSGSYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLBDSFSCTCPPGF 360
QY 358 YGKVCSELSAMTCADGCFNGGRCSDNPDGGYTCCHPLGFSGENCEKMDLCCSSPSCNGA 417
Db 361 YGKNCSELSAMTCADGCFNGGRCSDNPDGGYTCCHPLGFSGENCEKMDLCCSSPSCNGA 420
QY 418 KCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCCANGGTTCRDSVNDVDFCTCPPGYTGKNC 477
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QY 478 SAPVSRCEHAPCHNGATCHQGRQVWCECAQYGGPNCQFLPPEPPPGMVVDLSRRHME 537
Db 481 SMPITKCEHNPCHNGATCHERNRYVCCARGYGNQCFLLPEEK--PVVVDLTKYTE 538
QY 538 SQGGPPWVAVCAGVVLVLLGLGCAAVVVCVRLKLQKHOPPEPCGGSETETMNNLANCQ 597
Db 539 SQGGPPWVAVCAGVVLVLLGLGCAAVVVCVRLKLQKHOPPEPCGGSETETMNNLANCQ 598
QY 598 REKOVSVSIIIGATQIKNTNKKADPHDGHAEKSSPKVRYPTVDYNLVRDLKDEATVRDT 657
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Db 658 RSKCEAKGSSNDSSESVNHSKRDSE-----RRRDSAYSTSKDYQSVYVI 708
QY 710 SAEKDECIATEV 722
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RESULT 15
US-08-872-855-7
; Sequence 7, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-855-7

Query Match 76.7%; Score 3161.5; DB 3; Length 721;
Best Local Similarity 72.7%; Pred. No. 2.1e-229;
Matches 533; Conservative 89; Mismatches 88; Indels 23; Gaps 5;

QY 1 MGRSALALAVVSALLQVWSSGVFELKLOBFVNKGLLGNRNCCRGSGPP---CACRT 57
DB 1 MGQRMTLVLVLSAVLQISCSGLFELRLQEFVNKGLLGNRNCCRGSLASLQRCCKT 60

QY 58 FFRVCLXHYQASVSPPECTYGSVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPG 117
DB 61 FFRICLXHYQSNVSPPECTYGGAVTPVLGTNSFVVPSSNADPTFSNPIRFPFGFTWPG 120

QY 118 TFSLIIEALHTDSDPDLATENPERLISRLTORHLTVGBEWSQDLHSSGRTDLAYSIRFV 177
DB 121 TFSLIIEAHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSIRFV 180

QY 178 CDEHYGEGCSVFCRRDDAFHFTCTGDRGKMDPGMKGOYCTDPICLPGCDDQHGICYD 237
DB 181 CDEYIYEGGSDYCRPRDDAFHFPSCGKGNLCPGWKGLYCTEPICLPGCDEHHGYCD 240

QY 238 KPGECKCRVGMQGRYCDICIRYPCGVHGTQQPWCNCQCGWGLFCNQDLNYCTHHKPC 297
DB 241 KPGECKCRVGMQGRYCDICIRYPCGLAGTQQPWCNCQCGWGLFCNQDLNYCTHHKPC 300

QY 298 RRGATCTNTGGSYTCSCRGYTGANCELEVEDECAPSKNGASCTDLESFSCTCPGPF 357
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QY 358 YGKVCESLMTADGCPGFCNGRCDNPDGTYCHCLPGFSGNCEKKNWDLGSSPCSNGA 417
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DB 421 RCEDLGNLYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPSCTCPGYTGKNC 480

QY 478 SAPVSRCEHAPCHNGATCHQGRGYMCECAQGYGPNQCQLLPEPPPGMVVDLSERHME 537
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QY 538 SQGGPPPWAVACGVVLVLLLLGCAAVVYVRLKQHQPPPEPCGGETETMNNLANCO 597
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QY 598 REKDVSIIICATQIKNTNKKADPHGDHGAESKSFVRYPTVDYVNLVRLDKGDEATVRDT 657
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QY 658 HSKRDTKQCS-----QSLQKGRSPQHLGVGRFLTENRPSVYSTSKDTKYQSVYVL 709
DB 658 RSKCEAKCSSDSDSVNSVHKSRRDSE-----RRRPDSAYSTSKDTKYQSVYVI 708

QY 710 SAEKDECVIATEV 722
DB 709 SDEKDECIATEV 721

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:26:20 ; Search time 72.7322 Seconds
(without alignments)
3520.994 Million cell updates/sec

Title: US-09-783-931-12

Perfect score: 4121

Sequence: 1 MGRSALALWASALLCQVW.....YQSVYVLSAEKDECVIATEV 722

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Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4003	97.1	722	15	US-10-042-865-107
4	4003	97.1	722	16	US-10-731-741-4
5	3971	96.4	720	14	US-10-417-719-4
6	3848	93.4	714	15	US-10-042-865-108
7	3840.5	93.2	713	14	US-10-417-719-5
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ALIGNMENTS

RESULT 1

US-09-908-322-12

Sequence 12, Application US/09908322

Patent No. US20020107194A1

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David

Henrique, Domingos Manuel Pinto

Lewis, Julian Hart

Artavanis-Tsakonas, Spyridon

Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF

VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION NUMBER: US/09/908,322

APPLICATION DATA:

FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-908-322-12

Query Match      100.0%; Score 4121; DB 9; Length 722;
Best Local Similarity 100.0%; Pred. No. 4.3e-272;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSALALAVVSALLCQVSSGVFELKIQEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
DB 1 MGRSALALAVVSALLCQVSSGVFELKIQEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
QY 61 VCLKHQYQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTFS 120
DB 61 VCLKHQYQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTFS 120
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180
QY 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMDPQWKGQYCTDPICLPGCDDQHGVCDEKPG 240
DB 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMDPQWKGQYCTDPICLPGCDDQHGVCDEKPG 240
QY 241 ECKCRVGMQGRYCDCEIRYPGCVHGTGCOQWQNCQEGWGLFCNQDLNYCTHHKPCRNG 300
DB 241 ECKCRVGMQGRYCDCEIRYPGCVHGTGCOQWQNCQEGWGLFCNQDLNYCTHHKPCRNG 300
QY 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTCPGFGYK 360
DB 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTCPGFGYK 360
QY 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGFNCKRMDLCSGSPCSNGAKCV 420
DB 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGFNCKRMDLCSGSPCSNGAKCV 420
QY 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGPGYTGKNCSP 480
DB 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGPGYTGKNCSP 480
QY 481 VSRCEHAPCHNGATQHQRQRYMCECAQYGGPNCQFLPBPDPGPMVVDLSERHMSQG 540
DB 481 VSRCEHAPCHNGATQHQRQRYMCECAQYGGPNCQFLPBPDPGPMVVDLSERHMSQG 540
QY 541 GPPFPAVAVCAGVVLVLLLLGCAAVVVRLLKQHQPPPEPCGGGTETMNNLANCOREK 600
DB 541 GPPFPAVAVCAGVVLVLLLLGCAAVVVRLLKQHQPPPEPCGGGTETMNNLANCOREK 600
QY 601 DVSVSIIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDATVRDTHSK 660
DB 601 DVSVSIIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDATVRDTHSK 660
QY 661 RDTKQSQSLQEKRRSPQHLGVGRFLTENRPSVSTSTKDTKYQSVYVLSAEKDECVIAT 720
DB 661 RDTKQSQSLQEKRRSPQHLGVGRFLTENRPSVSTSTKDTKYQSVYVLSAEKDECVIAT 720
QY 721 EV 722
DB 721 EV 722
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; Sequence 12, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Igh-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Taakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-783-931-12
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Query Match      100.0%; Score 4121; DB 10; Length 722;
Best Local Similarity 100.0%; Pred. No. 4.3e-272;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSALALAVVSALLCQVSSGVFELKIQEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
DB 1 MGRSALALAVVSALLCQVSSGVFELKIQEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
QY 61 VCLKHQYQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTFS 120
DB 61 VCLKHQYQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTFS 120
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180
QY 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMDPQWKGQYCTDPICLPGCDDQHGVCDEKPG 240
DB 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMDPQWKGQYCTDPICLPGCDDQHGVCDEKPG 240
QY 241 ECKCRVGMQGRYCDCEIRYPGCVHGTGCOQWQNCQEGWGLFCNQDLNYCTHHKPCRNG 300
DB 241 ECKCRVGMQGRYCDCEIRYPGCVHGTGCOQWQNCQEGWGLFCNQDLNYCTHHKPCRNG 300
QY 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLEDSFSCCTCPGFGYK 360
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Db 301 ATCTNTGSGYTCSRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCCTCPGFGYK 360
Qy 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFGFNCCKMDLGCSSPSCNGAKCV 420
Db 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFGFNCCKMDLGCSSPSCNGAKCV 420
Qy 421 DLGNSYLCRCQAGFSGRYCEBNDVDDCASSPCANGGTCTCRDSVNDFSCTCPGTYTGKNCAP 480
Db 421 DLGNSYLCRCQAGFSGRYCEBNDVDDCASSPCANGGTCTCRDSVNDFSCTCPGTYTGKNCAP 480
Qy 481 VSRCEHAPCHNGATCHORQORYMCECAQYCGPNQCQLLPEPPGPMVVDLSERHESQ 540
Db 481 VSRCEHAPCHNGATCHORQORYMCECAQYCGPNQCQLLPEPPGPMVVDLSERHESQ 540
Qy 541 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHOPPPPCGGETETMNLANCOREK 600
Db 541 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHOPPPPCGGETETMNLANCOREK 600
Qy 601 DVSVSIIGATQIKNTNKKADFHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Db 601 DVSVSIIGATQIKNTNKKADFHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Qy 661 RDTKQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVIAT 720
Db 661 RDTKQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVIAT 720
Qy 721 EV 722
Db 721 EV 722

RESULT 3

US-10-042-865-107
; Sequence 107, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenna
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09

; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-042-865-107

Query Match 97.1%; Score 4003; DB 15; Length 722;
Best Local Similarity 97.2%; Pred. No. 4.6e-264;
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGRSALALAVVSALLCQVMSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCACRTFFR 60
Db 1 MGRSALALAVVSALLCQVMSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCACRTFFR 60
Qy 61 VCLKHYQASVSPPECTYGSVAVTVLGVDSFSLPDGAGIDPAFNPINRPFPGFTWPGTFS 120
Db 61 VCLKHYQASVSPPECTYGSVAVTVLGVDSFSLPDGAGIDPAFNPINRPFPGFTWPGTFS 120
Qy 121 LIIEALHTSDPDDLATENPERLISRLTTQRLTVGEEWSQDLHSSGRTDLRSYRFPVUDE 180
Db 121 LIIEALHTSDPDDLATENPERLISRLTTQRLTVGEEWSQDLHSSGRTDLRSYRFPVUDE 180
Qy 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMCDCPKWGOYCTDPICLPGCDDQHGVCCKPG 240
Db 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMCDCPKWGOYCTDPICLPGCDDQHGVCCKPG 240
Qy 241 ECKRVGMQGRYCDCEIRYPCGVHGTCCQPMQNCQBGWGLFCNQDLNYCTHHKPCRNAG 300
Db 241 ECKRVGMQGRYCDCEIRYPCGVHGTCCQPMQNCQBGWGLFCNQDLNYCTHHKPCRNAG 300
Qy 301 ATCTNTGSGYTCSRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCCTCPGFGYK 360
Db 301 ATCTNTGSGYTCSRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCCTCPGFGYK 360
Qy 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFGFNCCKMDLGCSSPSCNGAKCV 420
Db 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFGFNCCKMDLGCSSPSCNGAKCV 420
Qy 421 DLGNSYLCRCQAGFSGRYCEBNDVDDCASSPCANGGTCTCRDSVNDFSCTCPGTYTGKNCAP 480
Db 421 DLGNSYLCRCQAGFSGRYCEBNDVDDCASSPCANGGTCTCRDSVNDFSCTCPGTYTGKNCAP 480
Qy 481 VSRCEHAPCHNGATCHORQORYMCECAQYCGPNQCQLLPEPPGPMVVDLSERHESQ 540
Db 481 VSRCEHAPCHNGATCHORQORYMCECAQYCGPNQCQLLPEPPGPMVVDLSERHESQ 540
Qy 541 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHOPPPPCGGETETMNLANCOREK 600
Db 541 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHOPPPPCGGETETMNLANCOREK 600
Qy 601 DVSVSIIGATQIKNTNKKADFHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Db 601 DVSVSIIGATQIKNTNKKADFHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Qy 661 RDTKQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVIAT 720
Db 661 RDTKQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVIAT 720
Qy 721 EV 722
Db 721 EV 722

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RESULT 4
US-10-731-741-4
; Sequence 4, Application US/10731741
; Publication No. US20040171148A1
; GENERAL INFORMATION:
; APPLICANT: Schmitt, Thomas M.
; APPLICANT: Zuniga-Pflucker, Juan-Carlos
; TITLE OF INVENTION: Cell Preparations Comprising Cells of the T Cell
; TITLE OF INVENTION: Lineage and Methods of Making and Using Them
; FILE REFERENCE: 2223-171
; CURRENT APPLICATION NUMBER: US/10/731,741
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432,525
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-731-741-4

Query Match      97.1%; Score 4003; DB 16; Length 722;
Best Local Similarity 97.2%; Pred. No. 4.6e-264;
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCACRTFFR 60
DB 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCACRTFFR 60
QY 61 VCLKHYQASVSEPPCTCYGSAVTPVLGVDSFSLPDGAGIDPAPSNPIRPFPGFTWPGTFS 120
DB 61 VCLKHYQASVSEPPCTCYGSAVTPVLGVDSFSLPDGAGIDPAPSNPIRPFPGFTWPGTFS 120
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRSYRFVCD 180
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRSYRFVCD 180
QY 181 HYYGEGSVFCRPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDDOHGYCDKPG 240
DB 181 HYYGEGSVFCRPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDDOHGYCDKPG 240
QY 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPMQCNCEQWGGGLFCNQDLNYCTHHKPCRNG 300
DB 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPMQCNCEQWGGGLFCNQDLNYCTHHKPCRNG 300
QY 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLEDSEFSCCTPPGFYK 360
DB 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLEDSEFSCCTPPGFYK 360
QY 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGNCCKMDLGCSSSPCSNGAKCV 420
DB 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGNCCKMDLGCSSSPCSNGAKCV 420
QY 421 DLGNSYLCRCQAGFSGRYCEDNVDVDCASSPCANGGTCDRSVNDFSCTCPPGYTGKNCAP 480
DB 421 DLGNSYLCRCQAGFSGRYCEDNVDVDCASSPCANGGTCDRSVNDFSCTCPPGYTGKNCAP 480
QY 481 VSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLPPEPPGPMVVDLSERHMESQ 540
DB 481 VSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLPPEPPGPMVVDLSERHMESQ 540
QY 541 GPPPMVAVCAGVVLVLLLLLGCAAVVCVRLKLOKHQPPPECGGTETMNNLANCQREK 600
DB 541 GPPPMVAVCAGVVLVLLLLLGCAAVVCVRLKLOKHQPPPECGGTETMNNLANCQREK 600
QY 601 DVSVSIIIGATQIKNTNKKADFHDGHAESKSFVRYPTVDYDNLVRLDKGEATVRDTHSK 660
DB 601 DVSVSIIIGATQIKNTNKKADFHDGHAESKSFVRYPTVDYDNLVRLDKGEATVRDTHSK 660
QY 661 RDTKQSQSLQEKRRSFQHLGVGRFLTENRPESVYSTSKDTKYQSYVVLSAEKDECVIAT 720
DB 661 RDTKQSQSSAGEBKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSYVVLSAEKDECVIAT 720
```

```
QY 721 EV 722
DB 721 EV 722

RESULT 5
US-10-417-719-4
; Sequence 4, Application US/10417719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT APPLICATION NUMBER: US/10/417,719
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 08/672,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-417-719-4

Query Match      96.4%; Score 3971; DB 14; Length 720;
Best Local Similarity 97.0%; Pred. No. 6.9e-262;
Matches 700; Conservative 4; Mismatches 16; Indels 2; Gaps 2;

QY 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCACRTFFR 60
DB 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCACRTFFR 60
QY 61 VCLKHYQASVSEPPCTCYGSAVTPVLGVDSFSLPDGAGIDPAPSNPIRPFPGFTWPGTFS 120
DB 61 VCLKHYQASVSEPPCTCYGSAVTPVLGVDSFSLPDGAGIDPAPSNPIRPFPGFTWPGTFS 119
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRSYRFVCD 180
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGSEWSQDLHSSGRTDLRSYRFVCD 178
QY 181 HYYGEGSVFCRPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDDOHGYCDKPG 240
DB 179 HYYGEGSVFCRPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDDOHGYCDKPG 238
QY 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPMQCNCEQWGGGLFCNQDLNYCTHHKPCRNG 300
DB 239 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPMQCNCEQWGGGLFCNQDLNYCTHHKPCRNG 298
QY 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLEDSEFSCCTPPGFYK 360
DB 299 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLEDSEFSCCTPPGFYK 358
QY 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGNCCKMDLGCSSSPCSNGAKCV 420
DB 359 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGNCCKMDLGCSSSPCSNGAKCV 418
QY 421 DLGNSYLCRCQAGFSGRYCEDNVDVDCASSPCANGGTCDRSVNDFSCTCPPGYTGKNCAP 480
DB 419 DLGNSYLCRCQAGFSGRYCEDNVDVDCASSPCANGGTCDRSVNDFSCTCPPGYTGKNCAP 478
QY 481 VSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLPPEPPGPMVVDLSERHMESQ 540
DB 479 VSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLPPEPPGPMVVDLSERHMESQ 538
QY 541 GPPPMVAVCAGVVLVLLLLLGCAAVVCVRLKLOKHQPPPECGGTETMNNLANCQREK 600
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Db 539 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEFCGGETETMNNLANCOREK 598
Qy 601 DVSVSIIGATQIKNTNKKADPHGDHGAESKFVRYPTVDYNLVDLKGDEATVRDTHSK 660
Db 599 DVSVSIIGATQIKNTNKKADPHGDHGAESKFVRYPTVDYNLVDLKGDEATVRDTHSK 658
Qy 661 RDTKQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVIAT 720
Db 659 RDTKQSQSSAGEEIKAPTLAGGEIPDRKRPEVYSTSKDTKYQSVVYVLSAEKDECVIAT 718
Qy 721 EV 722
Db 719 EV 720

RESULT 6

US-10-042-865-108

; Sequence 108, Application US/10042865

; Publication No. US20040029216A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Li, Li

; APPLICANT: Zernhusen, Bryan D

; APPLICANT: Casman, Stacie J

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Spyttek, Kimberly

; APPLICANT: Zhong, Mei

; APPLICANT: Gangoli, Esha A

; APPLICANT: Burgess, Catherine E

; APPLICANT: Patturajan, Meera

; APPLICANT: Vernet, Corine A.M

; APPLICANT: Taylor, Sarah

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Miller, Charles E

; APPLICANT: Guo, Xiaojia

; APPLICANT: Boldog, Ference L

; APPLICANT: Grosbe, William M

; APPLICANT: Alsobrook II, John P

; APPLICANT: Gerlach, Valerie L

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Rothenberg, Mark E

; APPLICANT: Ellerman, Karen

; APPLICANT: MacDougall, John

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Millet, Teabelle

; APPLICANT: Peyman, John

; APPLICANT: Smithson, Glennda

; APPLICANT: Stone, David

; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

; FILE REFERENCE: 21402-537

; CURRENT APPLICATION NUMBER: US/10/042,865

; CURRENT FILING DATE: 2002-05-17

; PRIOR APPLICATION NUMBER: 60/260,417

; PRIOR FILING DATE: 2001-01-09

; PRIOR APPLICATION NUMBER: 60/260,831

; PRIOR FILING DATE: 2001-01-10

; PRIOR APPLICATION NUMBER: 60/272,338

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/274,876

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: 60/284,704

; PRIOR FILING DATE: 2001-04-18

; NUMBER OF SEQ ID NOS: 264

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 108

; LENGTH: 714

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-042-865-108

Query Match 93.4%; Score 3848; DB 15; Length 714;
Best Local Similarity 93.2%; Pred. No. 1.6e-253;
Matches 673; Conservative 13; Mismatches 28; Indels 8; Gaps 1;
Qy 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNNKGLLGNRNCRCGGSPPCACRTFFR 60
Db 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNNKGLLGNRNCRCGGSPPCACRTFFR 60
Qy 61 VCLKHYQASVSPPECTYGSATVPLGVDSFSLPDGAGIDPAFNPINRPFPGFTWPGTFS 120
Db 61 VCLKHYQASVSPPECTYGSATVPLGVDSFSLPDGAGIDPAFNPINRPFPGFTWPGTFS 120
Qy 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEMSQDLHSSGRTDLSYRVFVDE 180
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEMSQDLHSSGRTDLSYRVFVDE 180
Qy 181 HYYGEGSVFCRPRDDAFHFTCGDRGKMCDFGKQCYCTDDPICLPGCDDOHGYCDKPG 240
Db 181 HYYGEGSVFCRPRDDAFHFTCGDRGKMCDFGKQCYCTDDPICLPGCDDOHGYCDKPG 240
Qy 241 ECKRVGWQGRYCDCEIRYPCGVHGTQQPWCNCQEGWGLFCNQDLNYCTHHKPCRN 300
Db 241 ECKRVGWQGRYCDCEIRYPCGVHGTQQPWCNCQEGWGLFCNQDLNYCTHHKPCRN 300
Qy 301 ATCTNTGQSYTCSRPYTGANCELEVBECAPSPCKNGASCSTDLEDSFCTCPPGFYGK 360
Db 301 ATCTNTGQSYTCSRPYTGANCELEVBECAPSPCKNGASCSTDLEDSFCTCPPGFYGK 360
Qy 361 VCELSAMTCADGCFNGGRCSDNPDGGYTCHPLGFSGFNCEKMDLCSGSSPCSNKACV 420
Db 361 VCELSAMTCADGCFNGGRCSDNPDGGYTCHPLGFSGFNCEKMDLCSGSSPCSNKACV 420
Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGTCTCRDSVNDPSCTCPGYTGKNC 480
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGTCTCRDSVNDPSCTCPGYTGKNC 480
Qy 481 VSRCEHAPCHNGATCHQGRQYMCCEAQYGGNQCQFLLPEPPPMVVDLSERHMSQ 540
Db 481 VSRCEHAPCHNGATCHQGRQYMCCEAQYGGNQCQFLLPEPPPMVVDLSERHMSQ 540
Qy 541 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEFCGGETETMNNLANCOREK 600
Db 541 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEFCGGETETMNNLANCOREK 600
Qy 599 DVSVSIIGATQIKNTNKKADPHGDHGAESKFVRYPTVDYNLVDLKGDEATVRDTHSK 660
Db 599 DVSVSIIGATQIKNTNKKADPHGDHGAESKFVRYPTVDYNLVDLKGDEATVRDTHSK 652
Qy 661 RDTKQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVIAT 720
Db 653 RDTKQSQSGVGEKSTSTLRGGEVDPDRKRPEVYSTSKDTKYQSVVYVLSAEKDECVIAT 712
Qy 721 EV 722
Db 713 EV 714

RESULT 7

US-10-417-719-5

; Sequence 5, Application US/10417719

; Publication No. US20030180784A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc

; APPLICANT: McCarthy, Sean

; APPLICANT: Gearing, David

; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF

; FILE REFERENCE: MBIO1997-002CP2M

; CURRENT APPLICATION NUMBER: US/10/417,719

; CURRENT FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: US/09/568,218

; PRIOR FILING DATE: 2000-05-09

; PRIOR APPLICATION NUMBER: 08/872,855

; PRIOR FILING DATE: 1997-06-11

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; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Rattus No. US20030180784Alveigicus
US-10-417-719-5

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Best Local Similarity 93.4%; Pred. No. 5.2e-253;
Matches 674; Conservative 11; Mismatches 28; Indels 9; Gaps 2;

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DB 1 MGRSALALAVVSALLCQWSSGVFELKLOEFVNKGLGNRNCRCGGSGPPCACRTTFR 60
QY 61 VCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNPDIRFPFGTWPGTFS 120
DB 61 VCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNPDIRFPFGTWPGTFS 120
QY 121 LIIELHTDSPDLATENPERLISRLTQRLHVTGEEWSQDLHSSGRTDLRSYRFVCD 180
DB 121 LIIELHTDSPDLATENPERLISRLTQRLHVTGEEWSQDLHSSGRTDLRSYRFVCD 179
QY 181 HYYGEGSVFCRPRDDAFGHFTCGRGEKMDPGWKGOYCTDPICLPGCDDQHGVCXDP 240
DB 181 HYYGEGSVFCRPRDDAFGHFTCGRGEKMDPGWKGOYCTDPICLPGCDDQHGVCXDP 239
QY 180 HYYGEGSVFCRPRDDAFGHFTCGRGEKMDPGWKGOYCTDPICLPGCDDQHGVCXDP 239
QY 241 ECKRCVGMQGRYCDCEIRYPGCVHGTGQCPWQCNQCEGMLFCNQDLNYCTHHKPCRN 300
DB 240 ECKRCVGMQGRYCDCEIRYPGCVHGTGQCPWQCNQCEGMLFCNQDLNYCTHHKPCRN 299
QY 301 ATCTNTGQSGYTCSCRPYTGANCELEVDDECAPSPCKNGASCTDLEDSPSCCTPPGFYK 360
DB 300 ATCTNTGQSGYTCSCRPYTGANCELEVDDECAPSPCKNGASCTDLEDSPSCCTPPGFYK 359
QY 361 VCELSAMTADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKMDLCSGSSPCSNAGKCV 420
DB 360 VCELSAMTADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKMDLCSGSSPCSNAGKCV 419
QY 421 DLGNSYLRCQAGSRYCEDNVDVDCASSPCANGGTCDRSVNDFSCTCPGPGYTKNCSAP 480
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QY 481 VSRCEHAPCHNGATCHQORGYMCECAQGYGPNCOFLPEPPPMVVDLSERHMSQ 540
DB 480 VSRCEHAPCHNGATCHQORGYMCECAQGYGPNCOFLPEPPPMVVDLSERHMSQ 531
QY 541 GPPFWAVACAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETETMNNLANCQREK 600
DB 532 GSPFWAVACAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETETMNNLANCQREK 591
QY 601 DVSVSIIIGATQIKNTNKKADFGHDGAEKSPKRYPTVDYNLVRDLKGDATVRDTHSK 660
DB 592 DVSVSIIIGATQIKNTNKKADFGHDGAEKSPKRYPTVDYNLVRDLKGDATVRDTHSK 651
QY 661 RDTKCSQSLQEKRRSPQHLGVRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
DB 652 RDTKCSQSGSAGEKSTSLRGGEVDPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 711
QY 721 EV 722
DB 712 EV 713

Query Match      88.8%; Score 3659.5; DB 9; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRSALALAVVSALLCQWSSGVFELKLOEFVNKGLGNRNCRCGGSG-PPCACRTTFF 59
DB 1 MGRSALALAVVSALLCQWSSGVFELKLOEFVNKGLGNRNCRCGGSG-PPCACRTTFF 60
QY 60 RVCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNPDIRFPFGTWPGTFF 119
DB 61 RVCLKHQASVSPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFNPDIRFPFGTWPGTFF 120
QY 120 SLIIELHTDSPDLATENPERLISRLTQRLHVTGEEWSQDLHSSGRTDLRSYRFVCD 179
DB 121 SLIIELHTDSPDLATENPERLISRLTQRLHVTGEEWSQDLHSSGRTDLRSYRFVCD 180
QY 180 EHYGEGSVFCRPRDDAFGHFTCGRGEKMDPGWKGOYCTDPICLPGCDDQHGVCXDP 239
DB 181 EHYGEGSVFCRPRDDAFGHFTCGRGEKMDPGWKGOYCTDPICLPGCDDQHGVCXDP 240
QY 240 GECKRVGMQGRYCDCEIRYPGCVHGTGQCPWQCNQCEGMLFCNQDLNYCTHHKPCRN 299
DB 241 GECKRVGMQGRYCDCEIRYPGCVHGTGQCPWQCNQCEGMLFCNQDLNYCTHHKPCRN 300
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DB 301 GATCTNTGQSGYTCSCRPYTGANCELEVDDECAPSPCKNGASCTDLEDSPSCCTPPGFYK 360
QY 360 KYCELSAMTADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKMDLCSGSSPCSNAGKAC 419
DB 361 KYCELSAMTADGCPFCNGRCSDNPDGGYTCPCPLGSGFNCCKMDLCSGSSPCSNAGKAC 420
QY 420 VDLGNSYLRCQAGSRYCEDNVDVDCASSPCANGGTCDRSVNDFSCTCPGPGYTKNCSA 479
DB 421 VDLGNSYLRCQAGSRYCEDNVDVDCASSPCANGGTCDRSVNDFSCTCPGPGYTKNCSA 480
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DB 481 PYSRCEHAPCHNGATCHQORGYMCECAQGYGPNCOFLPEPPPMVVDLSERHMSQ 539
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DB 600 KDVSVSIIIGATQIKNTNKKADFGHDGAEKSPKRYPTVDYNLVRDLKGDATVRDTHS 659
QY 660 KEDTKCSQ-SLOEKRRSPQHLGVRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 718
DB 660 KEDTKCSQ-SLOEKRRSPQHLGVRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 719
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RESULT 8

US-09-828-366-21

; Sequence 21, Application US/09828366

; Patent No. US2002010137A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

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; GENERAL INFORMATION:							
; APPLICANT: SAKANO, SEIJI							
; APPLICANT: ITOH, AKIRA							
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE							
; FILE REFERENCE: KP8447DIV							
; CURRENT APPLICATION NUMBER: US/09/995,593A							
; CURRENT FILING DATE: 2002-02-28							
; PRIOR APPLICATION NUMBER: 09/068,740							
; PRIOR FILING DATE: 1998-06-18							
; PRIOR APPLICATION NUMBER: JP 7-299611							
; PRIOR FILING DATE: 1995-11-17							
; PRIOR APPLICATION NUMBER: JP 7-311811							
; PRIOR FILING DATE: 1995-11-30							
; PRIOR APPLICATION NUMBER: PCT/JP96/03356							
; PRIOR FILING DATE: 1996-11-15							
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US-09-995-593A-9							
Query Match 88.8%; Score 3659.5; DB 9; Length 723;							
Best Local Similarity 87.0%; Pred. No. 1.1e-240;							
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;							
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Db	60	RVLCKHYQASVPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNIRPPFGTWPCTF	119		60	RVLCKHYQASVPEPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNIRPPFGTWPCTF	120
Qy	120	SLIIIEALHTSDPDLATENPERLSRLTQRHLTVGEEMSQDLHSSGRDLDLRYSRFVCD	179		120	SLIIIEALHTSDPDLATENPERLSRLTQRHLTVGEEMSQDLHSSGRDLDLRYSRFVCD	180
Db	180	EHYVGECSVFCRPRDDAFGHTCDGRGKMCDPGWKQYCTDPICLPGCDDQHGCDKP	239		180	EHYVGECSVFCRPRDDAFGHTCDGRGKMCDPGWKQYCTDPICLPGCDDQHGCDKP	240
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144 ; PRIOR FILING DATE: 1998-07-07

Query Match

88.8%; Score 3659.5; DB 14; Length 723;

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Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

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Db 1 MGRSALALAVVALLCQVWSSGVFELKIQEFVKNKGLGNRNCRCGSG-PPCACRTFF 60
Qy 60 RVCLKHQOASVSPPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGTWPQTF 119
Db 61 RVCLKHQOASVSPPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGTWPQTF 120
Qy 120 SLIIEALHTDSPDLATENPERLISRLTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 179
Db 121 SLIIEALHTDSPDLATENPERLISRLTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180
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Db 181 EHYGEGCSVFCPRDDAFGHFTCGDRGECMCDPMKGOYCTDPICLPGCDQHGDCDKP 240
Qy 240 GECKCRVGMQGRYDCIRYPCVHGTCQCPWQCNCQEGMGLFCNODLNYCTHHKPCRN 299
Db 241 GECKCRVGMQGRYDCIRYPCVHGTCQCPWQCNCQEGMGLFCNODLNYCTHHKPCRN 300
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Qy 360 KVCLESAWTCADGCPFNCGRCSDNPDGGYTCHCPGLFSGFNCCKMDDLCSGSSPCSNAGK 419
Db 361 KICELSAWTCADGCPFNCGRCSDNPDGGYTCHCPGLFSGFNCCKMDDLCSGSSPCSNAGK 420
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Qy 719 ATEV 722
Db 720 ATEV 723

RESULT 11
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; Sequence 346, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowaki, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
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; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-808-346

Query Match 88.8%; Score 3659.5; DB 14; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

Qy 1 MGRSALALAVVALLCQVWSSGVFELKIQEFVKNKGLGNRNCRCGSG-PPCACRTFF 59
Db 1 MGRSALALAVVALLCQVWSSGVFELKIQEFVKNKGLGNRNCRCGSG-PPCACRTFF 60
Qy 60 RVCLKHQOASVSPPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGTWPQTF 119
Db 61 RVCLKHQOASVSPPEPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGTWPQTF 120
Qy 120 SLIIEALHTDSPDLATENPERLISRLTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 179
Db 121 SLIIEALHTDSPDLATENPERLISRLTQRLHVTGSEWSQDLHSSGRTDLRYSYRFVCD 180
Qy 180 EHYGEGCSVFCPRDDAFGHFTCGDRGECMCDPMKGOYCTDPICLPGCDQHGDCDKP 239
Db 181 EHYGEGCSVFCPRDDAFGHFTCGDRGECMCDPMKGOYCTDPICLPGCDQHGDCDKP 240
Qy 240 GECKCRVGMQGRYDCIRYPCVHGTCQCPWQCNCQEGMGLFCNODLNYCTHHKPCRN 299
Db 241 GECKCRVGMQGRYDCIRYPCVHGTCQCPWQCNCQEGMGLFCNODLNYCTHHKPCRN 300
Qy 300 GATCTNTGQSGYTCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLDSFSCCTPPGFGY 359
Db 301 GATCTNTGQSGYTCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLDSFSCCTPPGFGY 360
Qy 360 KVCLESAWTCADGCPFNCGRCSDNPDGGYTCHCPGLFSGFNCCKMDDLCSGSSPCSNAGK 419
Db 361 KICELSAWTCADGCPFNCGRCSDNPDGGYTCHCPGLFSGFNCCKMDDLCSGSSPCSNAGK 420
Qy 420 VDLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFCCTCPGYTGKNCSA 479
Db 421 VDLGDAYLRCQAGFSGRHCDNDVDDCASSPCANGGTCRDSVNDPFCCTCPGYTGKNCSA 480
Qy 480 PVSRCCEHAPCHNGATCHQRGORYNCECAQYGGGNCQFLLPPEPPGMVVDLSRRHMSQ 539
Db 481 PVSRCCEHAPCHNGATCHQRGORYNCECAQYGGGNCQFLLPPEPPGMVVDLSRRHMSQ 539
Qy 540 GGPFPWAVACAGVILVLLMLLGGCAAVVVCVRLKQKHOPPEPCGGTETMNNLANCORE 599
Db 540 GGPFPWAVACAGVILVLLMLLGGCAAVVVCVRLKQKHOPPEPCGGTETMNNLANCORE 599
Qy 600 KDVSISIIGATQIKNTNKKADFHGDHGAESKFKVRYPTVDYVNLVRLDKGDEATVRDTHS 659
Db 600 KDVSISIIGATQIKNTNKKADFHGDHGAESKFKVRYPTVDYVNLVRLDKGDEATVRDTHS 659
Qy 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPSVYSTSKDTKYQSVYVLSAEKDECVI 718
Db 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPSVYSTSKDTKYQSVYVLSAEKDECVI 718
Qy 719 ATEV 722
Db 720 ATEV 723
```

```
RESULT 12
US-10-121-049-346
; Sequence 346, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-346

Query Match      88.8%; Score 3659.5; DB 14; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240; Indels 3; Gaps 3;
Matches 630; Conservative 46; Mismatches 45;

QY 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKKGLGNRCRCGGSG-PPCACRTFF 59
DB 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKKGLGNRCRCGGAGPPCACRTFF 60
QY 60 RVCLKHYQASVSPPECTYGSATPVLVGVDLSLDPGAGIDPAFNPPIRPFPGFTWPGTF 119
DB 61 RVCLKHYQASVSPPECTYGSATPVLVGVDLSLDPGAGIDPAFNPPIRPFPGFTWPGTF 120
QY 120 SLIIIEALHTDSDPDLATENPERLISRLTTORHLTVGEEWSQDLHSSGRDRLAYSVRFVCD 179
DB 121 SLIIIEALHTDSDPDLATENPERLISRLTTORHLTVGEEWSQDLHSSGRDRLAYSVRFVCD 180
QY 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDQHGXYCDXP 239
DB 181 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDQHGXYCDXP 240
QY 240 GECKRVGQGRYDCIRIYPCGVHGTCCQPMQCNQCEGNGGLFCNQDLNLYCTHHKPCRN 299
DB 241 GECKRVGQGRYDCIRIYPCGVHGTCCQPMQCNQCEGNGGLFCNQDLNLYCTHHKPCRN 300
QY 300 GATCTNTGGSYTCSCRPGYGTGANCELEVDCAKPSCKNGASCTDLEDSFSTCTCPGFGY 359
DB 301 GATCTNTGGSYTCSCRPGYGTGATCELGIDECDDPSCKNGGSCDLDUENSISTCTCPGFGY 360
QY 360 KVCLSAMTCADGCFNGRCSDNPDPGYTCHCPLGFSGFNCEKMDLCCGSPSCNGAKC 419
DB 361 KVCLSAMTCADGCFNGRCSDSPGGYSCRCPCVGYSGFNCEKKIDYCSSPSCNGAKC 420
QY 420 VDLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGKNCSA 479
DB 421 VDLGDAYLRCQAGFSGRHCDDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGKNCSA 480

QY 480 PVSRCHEAPCHNGATCHORGYMCECAQGYGPNQCQLLPEPPPPGPMVVDLSERHMSQ 539
DB 481 PVSRCHEAPCHNGATCHERGHRYVCECARGYGGPNQCQLLPELPGPVAVDITEK-LEQ 539
QY 540 GGPFPWAVACAGVILVLLGCAAIVVVCVRLKLOKHQPPPPPPCGGETTMNLANCQRE 599
DB 540 GGPFPWAVACAGVILVLLGCAAIVVVCVRLKLOKHQPPPPPPCGGETTMNLANCQRE 599
QY 600 KDVSYSIIIGATQIKNTNKKADPHGDHGAESKSPKYRYPTVDYVRLDKGDEATVRDTHS 659
DB 600 KDVSYSIIIGATQIKNTNKKADPHGDHGAESKSPKYRYPTVDYVRLDKGDEATVRDTHS 659
QY 660 KRDTCQSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTKDTKYQSVVVLSAEKDECVI 718
DB 660 KRDTCQSQSGSGEEKGTPTTLRGGEASERKRPDSCGCTSKDTKYQSVVVISEKDECVI 719
QY 719 ATEV 722
DB 720 ATEV 723

RESULT 13
US-10-123-904-346
; Sequence 346, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-346

Query Match      88.8%; Score 3659.5; DB 14; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240; Indels 3; Gaps 3;
Matches 630; Conservative 46; Mismatches 45;

QY 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKKGLGNRCRCGGSG-PPCACRTFF 59
DB 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKKGLGNRCRCGGAGPPCACRTFF 60
QY 60 RVCLKHYQASVSPPECTYGSATPVLVGVDLSLDPGAGIDPAFNPPIRPFPGFTWPGTF 119
DB 61 RVCLKHYQASVSPPECTYGSATPVLVGVDLSLDPGAGIDPAFNPPIRPFPGFTWPGTF 120
QY 120 SLIIIEALHTDSDPDLATENPERLISRLTTORHLTVGEEWSQDLHSSGRDRLAYSVRFVCD 179
DB 121 SLIIIEALHTDSDPDLATENPERLISRLTTORHLTVGEEWSQDLHSSGRDRLAYSVRFVCD 180
QY 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDQHGXYCDXP 239
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Db 181 EHYGEGCSVFCRPRDDAFGHFTCGERKEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240
Qy 240 GECKCRVWGQGRYDCECIRYPCGVHGTCCQWPQNCQEGWGLFCNQDLNCTTHHKPCRN 299
Db 241 GECKCRVWGQGRYDCECIRYPCGVHGTCCQWPQNCQEGWGLFCNQDLNCTTHHKPCRN 300
Qy 300 GATCTNTGQGSYTCSCRPGYTGCANGCELEVBDCAPSPCKNGASCTDLEDSFSCCTPPGFGY 359
Db 301 GATCTNTGQGSYTCSCRPGYTGCANGCELEVBDCAPSPCKNGASCTDLEDSFSCCTPPGFGY 360
Qy 360 KVCLSAMTADGCPFCNGRCSDNPDDGVTCHCPGFCGNCCKMDLCSGSSPCSNAGK 419
Db 361 KVCLSAMTADGCPFCNGRCSDNPDDGVTCHCPGFCGNCCKMDLCSGSSPCSNAGK 420
Qy 420 VDLGNSVLCRCQAGFSGRYCEBNDVDDCASSPCANGGTCRDSVNDPFCCTPPGYTGKNC 479
Db 421 VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDSVNDPFCCTPPGYTGKNC 480
Qy 480 PVSRCHEAPCHNGATCHORQRYMCECAQGYGPNCOFLLPEPPPGMVDLSRHHMESQ 539
Db 481 PVSRCHEAPCHNGATCHORQRYMCECAQGYGPNCOFLLPEPPPGMVDLSRHHMESQ 539
Qy 540 GGPFPWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGTETMNNLANCORE 599
Db 540 GGPFPWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGTETMNNLANCORE 599
Qy 600 KDVSVSIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659
Db 600 KDVSVSIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659
Qy 660 KRDTKCSQ-SLOEKRRSPQHLGVRFLTENRPSVYSTKDTKYQSVYVLSAEKDECVI 718
Db 660 KRDTKCSQ-SLOEKRRSPQHLGVRFLTENRPSVYSTKDTKYQSVYVLSAEKDECVI 719
Qy 719 ATEV 722
Db 720 ATEV 723

RESULT 14
US-10-140-470-346
; Sequence 346, Application US/10140470
; Publication No. US2003002231A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-140-470-346

Query Match 88.8%; Score 3659.5; DB 14; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;
Qy 1 MGRSALALAVVSALLQVWSSGVFELKLOEFVKNKGLLGNRNCRCGSG-PPACRTRFF 59
Db 1 MGRSALALAVLSALLQVWSSGVFELKLOEFVKNKGLLGNRNCRCGAGPPCACRTRFF 60
Qy 60 RVCLKHQVAVSPBPCTCYGSAVTPVLGVSFSLPDGGGADSAFNSPIRPFPGTWP 119
Db 61 RVCLKHQVAVSPBPCTCYGSAVTPVLGVSFSLPDGGGADSAFNSPIRPFPGTWP 120
Qy 120 SLIIEALHTSPDLDATENPERLISRLTTOHRLTVGEWSQDLHSSQDRLRYR 179
Db 121 SLIIEALHTSPDLDATENPERLISRLTTOHRLTVGEWSQDLHSSQDRLRYR 180
Qy 180 EHYGEGCSVFCRPRDDAFGHFTCGDRGKVCDFGKGOYCTDPICLPGCDDHGYCDK 239
Db 181 EHYGEGCSVFCRPRDDAFGHFTCGDRGKVCDFGKGOYCTDPICLPGCDDHGYCDK 240
Qy 240 GECKCRVWGQGRYDCECIRYPCGVHGTCCQWPQNCQEGWGLFCNQDLNCTTHHKPCRN 299
Db 241 GECKCRVWGQGRYDCECIRYPCGVHGTCCQWPQNCQEGWGLFCNQDLNCTTHHKPCRN 300
Qy 300 GATCTNTGQGSYTCSCRPGYTGCANGCELEVBDCAPSPCKNGASCTDLEDSFSCCTPPGFGY 359
Db 301 GATCTNTGQGSYTCSCRPGYTGCANGCELEVBDCAPSPCKNGASCTDLEDSFSCCTPPGFGY 360
Qy 360 KVCLSAMTADGCPFCNGRCSDNPDDGVTCHCPGFCGNCCKMDLCSGSSPCSNAGK 419
Db 361 KVCLSAMTADGCPFCNGRCSDNPDDGVTCHCPGFCGNCCKMDLCSGSSPCSNAGK 420
Qy 420 VDLGNSVLCRCQAGFSGRYCEBNDVDDCASSPCANGGTCRDSVNDPFCCTPPGYTGKNC 479
Db 421 VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDSVNDPFCCTPPGYTGKNC 480
Qy 480 PVSRCHEAPCHNGATCHORQRYMCECAQGYGPNCOFLLPEPPPGMVDLSRHHMESQ 539
Db 481 PVSRCHEAPCHNGATCHORQRYMCECAQGYGPNCOFLLPEPPPGMVDLSRHHMESQ 539
Qy 540 GGPFPWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGTETMNNLANCORE 599
Db 540 GGPFPWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGTETMNNLANCORE 599
Qy 600 KDVSVSIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659
Db 600 KDVSVSIIGATQIKNTNKKADFGHDGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659
Qy 660 KRDTKCSQ-SLOEKRRSPQHLGVRFLTENRPSVYSTKDTKYQSVYVLSAEKDECVI 718
Db 660 KRDTKCSQ-SLOEKRRSPQHLGVRFLTENRPSVYSTKDTKYQSVYVLSAEKDECVI 719
Qy 719 ATEV 722
Db 720 ATEV 723

RESULT 15
US-10-175-746-346
; Sequence 346, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-346

Query Match      88.8%; Score 3659.5; DB 14; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY      1 MGRSALALAVNSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRCGGSG-DEACRTEF 59
DB      1 MGRSALALAVNSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRCGGAGPPPCACRTEF 60

QY      60 RVCLKHQASVPEPPCTYGSATPVLVGDSFSLPDGAGIDPAFSNPIRPFPGFTWPGTF 119
DB      61 RVCLKHQASVPEPPCTYGSATPVLVGDSFSLPDGAGADSAFNSPIRPFPGFTWPGTF 120

QY      120 SLIIIEALHTDSPDDLATENPERLISRLTQRLHTVGEWSQDLHSSGRDRLYSYRFVCD 179
DB      121 SLIIIEALHTDSPDDLATENPERLISRLATQRLHTVGEWSQDLHSSGRDRLKYSYRFVCD 180

QY      180 EHYHGGCSVFCPRDDAFGHFTCGDRGERKMDPGWKQGYCTDPICLPGCDDQHGVCXDP 239
DB      181 EHYHGGCSVFCPRDDAFGHFTCGDRGERKVCNPNWKGYCTEPICLPGCDEQHGFCDXP 240

QY      240 GECKRVGHWQGRYCDRCIRYPGVCHGTCCQWQCNCQEGWGLFCNQDLNYCTHHKPCRN 299
DB      241 GECKRVGHWQGRYCDRCIRYPGLHGTCCQWQCNCQEGWGLFCNQDLNYCTHHKPCRN 300

QY      300 GATCTNTGGSVYTCSCRPGYTGANCELEVEDCAPSPCKNGASCTDLEDSEFSCTCPPGFYG 359
DB      301 GATCTNTGGSVYTCSCRPGYTGATCELGIDECDDPSCKNGGSCDLENSYSCTCPPGFYG 360

QY      360 KYCELSAMTCADGCPNGRCSDNPDGGYTCHCPLGFGFNCCKMDLCSGSPCSNGAKC 419
DB      361 KYCELSAMTCADGCPNGRCSDSPDGGYSCRCFVGYGFNCKEKIDYCSSSPCSNGAKC 420

QY      420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479
DB      421 VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPGYTGKNCSA 480

QY      480 PVSRCBHAPCHNGATQHQRGYMCECAQYGGPNCFLLPBPFPMPVVDLSERHMSQ 539
DB      481 PVSRCBHAPCHNGATCHERGHRYVCECARGYGGPNCFLLPELPPGPAVVDLTK-LEQG 539

QY      540 GGPFPWVAVCAGVVLVLLLLGCAAVVCLKQHPBPBPCGGCTETMNNLANCORE 599
DB      540 GGPFPWVAVCAGVILVLLLLGCAAVVVCVRLQKRPDPADPCRGETETMNNLANCORE 599

QY      600 KDVSIIIGATQIKNTNKKADPHGDHGAEKSPKRYPTVDYNLVRDLKGDATVRDTHS 659
DB      600 KDVSIIIGATQIKNTNKKADPHGDHSDXNGEKARYPAVDYNLVRDLKGDATVARDHS 659

QY      660 KRDTKQCSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYOSVYVLSAEKDECVI 718
DB      660 KRDTKQCPQSSGEKEGTPTTLRGGEASBRKRPDSGCGSTSKDTKYOSVYVISEEKDECVI 719
```

QY 719 ATEV 722
DB 720 ATEV 723

Search completed: November 29, 2004, 13:42:00
Job time : 74.7322 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:16:29 ; Search time 18.0943 Seconds
(without alignments)
3839.238 Million cell updates/sec

Title: US-09-783-931-12

Perfect score: 4121

Sequence: 1 MGRRSALALAVVSALLCQVM.....YQSYVILSAEKDECVIATEV 722

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4003	97.1	722	2 I48324	DELTA-like 1 - mou
2	3368	81.7	728	2 I50719	C-Delta-1 - chicke
3	1879.5	45.6	685	2 JC7570	Delta-4 protein -
4	1828	44.4	686	2 JC7559	Delta-4 protein -
5	1468.5	35.6	833	2 S19087	gene Delta protein
6	1463.5	35.5	832	2 A31246	neurogenic protein
7	1463.5	35.5	880	2 S00670	neurogenic repeat
8	1312	31.8	1220	2 A56136	jagged protein pre
9	1130	27.4	1408	2 S16148	gene serrate prote
10	810	19.7	2524	2 A35844	Xotch protein - Af
11	807.5	19.6	2531	2 A46019	notch-1 protein -
12	794.5	19.3	2531	2 S18188	notch protein homo
13	771	18.7	1064	2 A40136	fibropellin Ia - s
14	765.5	18.6	2437	2 S42612	transmembrane prot
15	761	18.5	1203	2 A49175	Notch B protein -
16	761	18.5	2471	2 A49128	cell-fate determin
17	759	18.4	2555	2 A40043	notch protein homo
18	756	18.3	2352	2 T30201	Notch homolog prot
19	753	18.3	2531	2 T31070	notch homolog - se
20	747	18.1	2321	2 S78549	notch3 protein - h
21	747	18.1	2703	1 A24420	notch protein - fr
22	742	18.0	2318	2 S45306	notch 3 protein - f
23	711	17.3	2139	2 A35672	crumbs protein - f
24	702.5	17.0	1964	2 T09059	notch4 - mouse
25	698	16.9	861	2 A48825	Notch homolog Motc
26	682	16.5	570	2 A48836	fibropellin C prec
27	632	15.3	1372	2 T25933	hypothetical prote
28	628	15.2	385	2 S53718	homeotic protein d
29	623	15.1	473	2 A56175	adhesive plaque pr

30	621.5	15.1	385	2 A54785	preadipocyte facto
31	601.5	14.6	1429	2 S06434	homeotic protein 1
32	596	14.5	383	2 S53716	delta-like homeoti
33	578.5	14.0	1295	2 A32901	glp1 protein precu
34	570.5	13.8	1469	2 A36665	slit protein 2 pre
35	570.5	13.8	1480	2 A36665	slit protein 1 pre
36	567	13.8	1531	2 T42218	protein FlilC7.4 (i
37	566	13.7	1722	2 E89753	protein FlilC7.4 (i
38	550.5	13.4	308	2 JC7125	epidermal growth f
39	538	13.1	601	2 T22025	hypothetical prote
40	538	13.1	601	2 D89711	protein F40E10.4 (
41	535	13.0	1687	2 T30176	EGF repeat transme
42	519.5	12.6	1025	2 T42626	secreted leucine-r
43	511.5	12.4	1523	2 T13953	MEGF5 protein - ra
44	489	11.9	387	2 B49175	Motch A protein -
45	462	11.2	3623	2 T08618	intrinsic factor-B

ALIGNMENTS

RESULT 1

I48324

DELTA-like 1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48324

R:Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Goessler, A.

Development 121, 2407-2418, 1995

A:Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin

A:Reference number: I48324; MUID:95401858; PMID:7671806

A:Accession: I48324

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-722 <RES>

A:Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g806569; PIDN:CAA56865.1; PID:g8065

C:Genetics:

A:Gene: Dll1

C:Superfamily: delta-4 protein; EGF homology

F;311-362/Domain: EGF homology <EGF2>

F;446-477/Domain: EGF homology <EGF>

F;484-515/Domain: EGF homology <EGF1>

Query Match 97.1%; Score 4003; DB 2; Length 722;

Best Local Similarity 97.2%; Pred. No. 1.1e-240;

Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGRRSALALAVVSALLCQVMSSGVFELKQEFVNKKGLLGNRNCRCGSGPPCACRTFFR 60

Db 1 MGRRSALALAVVSALLCQVMSSGVFELKQEFVNKKGLLGNRNCRCGSGPPCACRTFFR 60

Qy 61 VCLKHVQASVSPPPCTYGSATVPLGVDSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFES 120

Db 61 VCLKHVQASVSPPPCTYGSATVPLGVDSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFES 120

Qy 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRDLYSYRFFVCDE 180

Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRDLYSYRFFVCDE 180

Qy 181 HYEGGCVSFCRRDDAFHFTCGDRGKMCDCPGWKQGYCTDPTCLPGCDDQHQYCDKPG 240

Db 181 HYEGGCVSFCRRDDAFHFTCGDRGKMCDCPGWKQGYCTDPTCLPGCDDQHQYCDKPG 240

Qy 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPCQNCQSGGGLFCNQDLNCTHHKPCRN 300

Db 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPCQNCQSGGGLFCNQDLNCTHHKPCRN 300

Qy 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKPCXGASCTDLEDSFSCCTPPGFYGK 360

Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKPCXGASCTDLEDSFSCCTPPGFYGK 360

Qy 361 VCLSAMTCAADGCFNNGRCDNDPDGYTCHPLGFSGFNCKEKMVLCSGSSPCSNKACV 420

Db 361 VCLSAMTCAADGCFNNGRCDNDPDGYTCHPLGFSGFNCKEKMVLCSGSSPCSNKACV 420

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Db 361 VCELSAWTCADGFCFNGRCSDNPDGGYTCHCPLGFGNCEKMDLGGSSPCSNAGKCV 420
Qy 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPGGTGNKCSAP 480
Db 421 DLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPGGTGNKCSAP 480
Qy 481 VSRCEHAPCHNGATCHORQRYMCECAQGYGPNCOFLPPEPPGMVVDLSERHMESOG 540
Db 481 VSRCEHAPCHNGATCHORQRYMCECAQGYGPNCOFLPPEPPGMVVDLSERHMESOG 540
Qy 541 GFFPWPVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGTETMNNLANCQREK 600
Db 541 GFFPWPVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGTETMNNLANCQREK 600
Qy 601 DVSVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYNLVRDLKDEATVRDTHSK 660
Db 601 DVSVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYNLVRDLKDEATVRDTHSK 660
Qy 661 RDTKCQSLSQEKRRSPQHLGVRFLTENRPSVYSTSKDTKYQSVVLSAEKDECVIAT 720
Db 661 RDTKCQSLSQAGEKIAPTALRGGEIPDRKRPSVYSTSKDTKYQSVVLSAEKDECVIAT 720
Qy 721 EV 722
Db 721 EV 722

RESULT 2
I50719
C-Delta-1 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50719
R:Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A:Title: Expression of a Delta homologue in prospective neurons in the chick.
A:Reference number: I50719; MUID:95319507; PMID:7596411
A:Accession: I50719
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <HEN>
A:Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:g882411; PID:g8824
C:Superfamily: Delta-4 protein; EGF homology
F:299-332/Domain: EGF homology <EGX1>
F:339-370/Domain: EGF homology <EGF1>
F:416-447/Domain: EGF homology <EGX2>
F:454-485/Domain: EGF homology <EGF>
F:492-523/Domain: EGF homology <EGF3>
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Query Match 81.7%; Score 3368; DB 2; Length 728;
Best Local Similarity 78.5%; Pred. No. 2.4e-201;
Matches 574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;

Qy 1 MGRSALALAVVSALL--CQWSSGVFELKLOEFVNNKGLGNRNCCRGSGP-----P 52
Db 1 MGRFLLTLALSALLCRQVDGSGVFELKLOEFVNNKGLGNRNCCRG-GPGAGQQQ 59
Qy 53 CACRTFFRVLKHQASVSEPPCTTGYSAVTPVLGVDSFSLPGA-GIDPAFNSPIRFPF 111
Db 60 CDCKTFFRVLKHQASVSEPPCTTGYSAITPVLGANSFSPVDGAGGADPAFNSPIRFPF 119
Qy 112 GTWPGTFSLLIEALHTDSDPDLATENPERLLISRLTTORHLTVGEWSODLHSSGRTDLR 171
Db 120 GTWPGTFSLLIEALHTDSDPDLTENPERLLISRLATQRLHVLAGEWSODLHSSGRTDLK 179
Qy 172 YSYRFVCDHYHYGEGSVFCRPRDDAFGHFTCGDRGKMDPQWKGQYCTDIPICLPGCCD 231
Db 180 YSYRFVCDHYHYGEGSVFCRPRDDRFHFTCGERGEKVCNKGWKGQYCTEPICLPGCDE 239
Qy 232 QHGCDKPGCEKCRVWGQRYCDECTIRYPCGVHGTQQPQWQNCQBGWGLFCNQDLNYC 291
Db 240 QHGCDKPGCEKCRVWGQRYCDECTIRYPCGLHGTQQPQWQNCQBGWGLFCNQDLNYC 299
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Qy 292 THHKPCRNGATCTNTGQSYTCSCRPGYTGANCELEVEDCAPSPCKNGASCTDLEDSFSC 351
Db 300 THHKPCRNGATCTNTGQSYTCSCRPGYTGSCEIEINECDANPCKNGGSCSTDLENSYC 359
Qy 352 TCPPGFYGVKVCBELSAMTCADGFCFNGRCSDNPDGGYTCHCPLGFGNCEKMDLGGSS 411
Db 360 TCPPGFYGVKVCBELSAMTCADGFCFNGRCSDNPDGGYSCRCPLGYSGFNCEKKIDYCSS 419
Qy 412 PCSNGAKVDLGNLYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPG 471
Db 420 PCANGAQCVDLGNSYICQAGFTGRHCDNDVDDCASSPCVNGGTCQDGVNDYSCTCPPG 479
Qy 472 YTGKNCSPVSRCEHAPCHNGATCHORQRYMCECAQGYGPNCOFLPPEPPGMVVDL 531
Db 480 YNGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGLNCCQFLPPEPQGPVIVDF 539
Qy 532 SRHMESQGGPPWPVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGTETWN 591
Db 540 TEKYTEGQNSQFPWIAVCAGIILVLLMLLGGCAAVVVCVRLKVQKRHHQPEACRSETETWN 599
Qy 592 NLANCQREKDVSVSIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYNLVRDLKGBE 651
Db 600 NLANCQREKDISISVIGATQIKNTNKKVDHFHSDN-SDKNGYKRVYPSVDYNLVLHELK-NE 657
Qy 652 ATVRDTHSKRDTKCQSLSQEKRRSPQHLGVRFLTENRPSVYSTSKDTKYQSVVLSA 711
Db 658 DSVKBEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRKPSVYSTSKDTKYQSVVISE 717
Qy 712 EKDECVIATEV 722
Db 718 EKDECVIATEV 728

RESULT 3
JC7570
C-Delta-4 protein - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7570
R:Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A:Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A:Reference number: JC7569; MUID: 21064937; PMID:11134954
A:Accession: JC7570
A:Molecule type: mRNA
A:Residues: 1-685 <FON>
A:Cross-references: UNIPROT:Q9NR61; DDBJ:AB043894
C:Comment: This protein, a member of the Notch family of proteins, is a transmembrane rec
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C:Genetics:
A:Gene: delta-4
C:Superfamily: delta-4 protein; EGF homology
C:Keywords: transmembrane protein

Query Match 45.6%; Score 1879.5; DB 2; Length 685;
Best Local Similarity 48.6%; Pred. No. 3.7e-109;
Matches 363; Conservative 99; Mismatches 190; Indels 95; Gaps 23;

Qy 4 RSALALAVVSALLCQW-----SSGVFELKLOEFVNNKGLGNRNCCRGSGPPC--ACR 56
Db 6 RSASGALL--LLVALWQRAAGSGVFQLQLEFINERGVL-----ASGRPCPGCR 55
Qy 57 TFFRVLKHQASVSEPPCTTGYSAVTPVLGVDSFSLPD---CAGIDPAFNSPIRFPFG 113
Db 56 TFFRVLKHQFQAVVSP-GPCTFTGTSTPVLGTNSFAVRDSSGGG-----RNPLQLPFFNF 109
Qy 114 TWPGTFSLLIEALHTDSDPDLATENPERLLISRLTTORHLTVGEWSODLHSSGRTDLR 171
Db 110 TWPGTFSLLIEALHTDSDPDLATENPERLLISRLTTORHLTVGEWSODLHSSGRTDLR 168
Qy 172 YSYRFVCDHYHYGEGSVFCRPRDDAFGHFTCGDRGKMDPQWKGQYCTDIPICLPGCCD 231
Db 169 YSYRVICSDNYGDNCSRLCKRNDHFHGVYQCPDGNLSCLPFGWTGEYCCQIPICLSGCHE 228
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Qy	173	SYRFVCDHYHGGCSVFCRPRDADFHFHFTCGDGRGKMKCDPGWKGYCTDPICLPGCDDQ	233
Db	171	SYRVICSDNYGSGCSRLCKKKRHHFGHVEBCQPDGSLSCLPGMTGKYCDQPICLSGCHEQ	230
Qy	233	HGYCDRPGCECKRVGHQGRYCDRCIIRYPGCVHGTCCQPHQCNCQBGHGGGLFCNQDLNYCT	292
Db	231	NGVCSRPDEICIRPGWGRGLCNECIPHNGCRHGTCTSPMQACDEGSGGLFCDDQLNYCT	290
Qy	293	HHXPCRNAGATCTWTGGSYTCSCRPVGTGANCLEVEDECAPSCKPKNGASCCTDLEDSFSC	352
Db	291	HHSPCKNGSTCSNSGPKGYTCTCLPGYTGHEHCLGLSKASNPFCRNGSGCKQDENSYHCL	350
Qy	353	CPPEFYGVKVCESAMTCAADGCPFCNGRCSD-NPDGGYTHCPLGFGFNCCKKMDLCGSS	411
Db	351	CPPGYYGQHCHESTLTLCADSPCFNGGSCRRNQSSVACBCPNFTGSNCKEKKVDRCTSN	410
Qy	412	PCSNAGKVDLGNLYLCRCQAGSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG	471
Db	411	PCANGGQCQNRGSPSRTCRRPGFTGHCELHTISDCARSPCAHGSGTCHDLNENGVCVCTPAG	470
Qy	472	YTKGNKCSAPVSR--CEHAPCHNGATCHQ--RGORYMCECAQGYGGNCPGCFLLPEPPPGPM	527
Db	471	FSGRREVRITHDACASGCFNGATCTGLSPNNFVCPYGVFGVSRCEFPVGLPP----	526
Qy	528	VVDLSERHMBESOGGPPFWAVACVAGVVLVLLLLGLGCAAVVYVRLKLQKHQPPPEPCGGET	587
Db	527	-----SFFWAVAVSLGVLVLLVL-LVMVVAVR-QLRLRRPDDE----SR	566
Qy	588	ETMNNLANCOREKXDSVSIIGATQIKNTNKKADFHDGHAEKSSP-KVRYPTVDYNLVRD	646
Db	567	EAMNNLSDFQKD-----NLIPAAQLKNTNQKLEVEYDCLGDKNSCKQLQHTLTDYNLAPG	621
Qy	647	LKGDQATV-RDTHSKRDTCQSQSLQEKRRSPQHLGVGRFLTENRPE---SVYSTSKDTK	702
Db	622	LLRGGMPGKYPHS-----DKSLGEK-----VPLRLHSEKPECRISAICSPRDSM	666
Qy	703	QSYVYVLSAEKDECIATEV	722
Db	667	YQSVCLISBERNECIATEV	686

RESULT 5
 S19087
 gene Delta protein precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S19087
 R:Muskavitch, M.A.T.
 submitted to the EMBL Data Library, June 1991
 A:Reference number: S19087
 A:Accession: S19087
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-833 <MUS>
 A:Cross-references: UNIPROT:P10041; EMBL:Y00222
 C:Genetics:

A;Gene: FlyBase:DI
A;Cross-references: FlyBase:Fgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;335-371/Domain: EGF homology <EGFI>
F;378-415/Domain: EGF homology <EGXI>
F;457-488/Domain: EGF homology <EGP>
F;533-564/Domain: EGF homology <EGFJ>

Query Match 35.6%; Score 1468.5; DB 2; Length 833;
Best Local Similarity 39.9%; Pred. NO. 1.3e-83;
Matches 276; Conservative 91; Mismatches 229; Indels 95; Gaps 15;

Qy 11 VVSALLC-----QVSSGVFEKLQEFVNKGLGNRCRG---GSGPPC--ACRTFFR 60
 ::::| | | | | | | | | | | | | | | | | | | |
Db 7 LUTAFICFTVIQVHSSGSFEFLRLKYFSNDHRDNEGRCCSGESDGATGKCILGSKTRPR 66

A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;457-488/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>

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Query Match      35.5%; Score 1463.5; DB 2; Length 880;
Best Local Similarity 40.2%; Pred. No. 2.7e-83;
Matches 273; Conservative 95; Mismatches 240; Indels 71; Gaps 14;

Qy 11 VVSALLC-----QVSSGVFELKJQEFVNNKGLGNRNCRRG---GSGPPC--ACRTFFR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7  LLTAFICFTVIVQVHSSGSFELRLKYFSDNHRDNEGRCCSGESDAGTKGLGSKTRFR 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 VCLHXYQASVPEPCTGYSAVTPVLGVDSFSLPDGAGI-DPAFNSPIRFPFGTWPTTF 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 LCLHXYQATIDTTSQCTYGDVITPILGENSVNLTAQRFQNKGFNPFIQFFFSFWPGTF 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 120 SLIIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEBSODLHSSGRTDLRYSRVFVCD 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 SLIIEAHDHTNNSGNARTN-KLLTQRLVQVLEVSSEWTKNSQTSLEYDFRVTCDD 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 180 EHYEGEGSVFCRPRDDAFGHFTCDGRGKMCDFGKQGYCTDPICLPGCDDHGYCDKP 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 LNYVSGCAKFCRPRDDSFHSTCSETGEIILCTGWOQDYCHIPKCAKGC--EHGCDKP 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 240 GECKRVGWOGRYDCECIRYPCGVHGTCTQCPWQNCQBGWGLFCNQDLNCTHHKPCRN 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 NQVCQLGWKALCNECVLEPNCIHGTCKNPKWTICNIEGWGLYCNQDLNCTNHRPCKN 303
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 300 GATCNTGOGSYTCSRGPGYTGMANCELEVDSCAP--SPCKNGASCTD---LEDSCSTCP 354
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 GGTCTGTEGGLYTKCAPGYSGDDCENIYSCDADVPQCQGGTICIDPHHTKTKCHCR 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 355 PGFYGVKVCESAMTADGCFNGRCSDNPDG-----GYTCHPLGFGFNCCKMDLCL 408
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 NGWSGKMEKVLTKSDKPC-HQIGICRNVRFGLSGKGQGYCECPIGYSGFNCQLQDLC 422
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 409 GSSP-----CSNGAKVDLGNLYLCRCQAG 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 SPNFCINGSGSQPSGKICIPGSGFSGTRCTETNIDCLGHQCGENGGTICIDMVNYRCQCPG 482
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 434 PSRGYCEDNVDDCASSPCANGCTCRDVSVDNFSCTCPGTYTKNGCSAPVSRCEHAPCHNGA 493
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 FHGTHCSKVDLCLIRPCANGGTCLNLDNDYQCTCRAGFTGKDCSDVIDECSSGFCCHNGG 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 494 TCHQRGQRYMCECAQGYGPNCCQLFLPEPPPGPMVVDLSERHMSQG-----GPPFPWAV 548
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 TCMNRVNSFEVCVANGFRGKQCD---EESYDSVTFDAHQYGATTQARADGLANAQVVL 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 549 CAGVIVLVLILLGCAAVVVCVRLKQKHQPPPECGGETETNMNLANCQRE-KDVSVSII 607
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 599 AVFSVAMPLVAVIAACVVVFCMKRKRKRAQEKDNEARKQNEQNAVATMHNGSVAQVALA 658
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 608 GATQIKNTNKKADPHGDHG 626
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 659 SASMGKGTGNSGLTFDGG 677
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 8
A56136
jagged protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
C;Accession: A56136
R;Lindesell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
Cell 80, 909-917, 1995
A;Title: Jagged: a mammalian ligand that activates Notch1.
A;Reference number: A56136; MUID:95211842; PMID:7697721
A;Accession: A56136
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-1220 <LIN>
A;Cross-references: GB:L38483
F;379-410/Domain: EGF homology <EGF1>
F;492-523/Domain: EGF homology <EGF>
F;634-665/Domain: EGF homology <EGF2>

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Query Match      31.8%; Score 1312; DB 2; Length 1220;
Best Local Similarity 40.6%; Pred. No. 8.8e-74;
Matches 239; Conservative 78; Mismatches 215; Indels 56; Gaps 11;

Qy 2  GRRSALALAVSALLCOV-WSSGVFELKJQEFVNNKGLGNRNCRR---GSGPPC--CA-- 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 GRPLSLLLALLCALRAKAVCGASGQFEILISMQVNGELQNGCCABEGTLVRPYKCTRD 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 55 -CRTFFRVCLKHQYASVSPPECTGYSAVTPVLGVDSFSLPDGAGIDPAFNSPIRFPFGF 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 ECDTYFKVCLKBYOSRVTAGPCSFSGSGSTVEIGNTFNLKASRGND---RNRIVLPSF 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 114 TWPQTFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEBSODLHSSGRTDLAYS 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 AWPRSYTLVLEA--WDSND--TIQPSIIEKASHSGMINPSPROWTLKQNTGIAHFEYQ 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 174 YRFVCDHYEGEGSVFCRPRDDAFGHFTCDGRGKMCDFGKQGYCTDPICLPGCDDQH 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 IRVTCDDHYGYGFCGNKFCRPRDDFFGHYACDQNGNKTMEGMMGPECNKAICRQCSPKH 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 234 GYCDKPECKRCVWQGRYDCECIRYPCGVHGTCTQCPWQNCQBGWGLFCNQDLNCTH 293
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 GSCKLPGLDRCQYGMQLCYDKCLPHPGCVHGTCTNEMQCLCETNWGQLCDKQLNCGT 303
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 294 HKPCRNATCNTGOGSYTCSRGPGYTGMANCEL----- 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 HQPCLNRGTCSNTGPDYKQCSCEGYSGPNCIEAHACLSDPCHNRSGKETSSTSGFCEC 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 327 -----EVDECAPSPCKNGASCTDLEDSCSTCPGTYTKNGCSAPVSRCEHAPCHNGATC 375
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 SPGWGTGTCSTNIDDCSPNNCSHGCTCDLVNGFKVCPPQWTGKTCLQDANECEAKPCV 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 376 NGGRCSNDPGGYTCHPLGFGFNCCKMDLCSGSPCSNGCAKCVDLGNSVLCRCQAGFS 435
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 NARSCK-NLIASYCYDCLPGMNGQNCIDINID--LQCONDASCRDLVNGYRCICPPGYA 481
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 436 GRVCEDEVDDCASSPCANGCTCRDVSVDNFSCTCPGTYTKNGCSAPVSRCEHAPCHNGATC 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 482 GDHCERIDECASNPCLNGHCQNEINRFQCLCPTGFGSNLCQLDIDYCEBPNPCQNGAQC 541
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 496 HQRGQRYMCECAQGYGPNCCQLFLPEPPPGPM-VVDLSERHMSQGGP 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 542 YNRASDYFCKPEDYEGKNGSHLKDHCRTPPTCEVIDSCTVAMASNDTP 589
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 9
S16148
gene serrate protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16148; S16878; A36666
R;Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a co
A;Reference number: S16148; MUID:91347903; PMID:1840519
A;Accession: S16148
A;Molecule type: mRNA
A;Residues: 1-1408 <THO1>
A;Cross-references: UNIPROT:P18168; EMBL:X56811
R;Thomas, U.
submitted to the EMBL Data Library, November 1990
A;Reference number: S16878
A;Accession: S16878
A;Molecule type: mRNA
A;Residues: 1-1351,'T',1353-1408 <THO2>
A;Cross-references: EMBL:X56811; NID:g8563; PID:g8564

R:Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A:Title: The gene *Serrate* encodes a putative EGF-like transmembrane protein essential for
A:Reference number: A36666; MUID:91099666; PMID:2125287
A:Accession: A36666
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15,20-26,'A',28-1408 <PLE>
A:Cross-references: GB:M35759; NID:g158605; PID:g158606
C:Genetics:
A:Gene: FlyBase:Ser
A:Cross-references: FlyBase:FBgn0004197
C:Keywords: glycoprotein; transmembrane protein
F:1-84/Domain: signal sequence #status predicted <SIG>
F:85-1408/Product: gene serrate protein #status predicted <MAT>
F:85-1221/Domain: extracellular #status predicted <EXT>
F:283-316/Domain: EGF homology <EG01>
F:319-348/Domain: EGF homology <EG02>
F:355-388/Domain: EGF homology <EG03>
F:395-488/Domain: EGF homology #status atypical <EG04>
F:495-526/Domain: EGF homology <EG05>
F:533-608/Domain: EGF homology #status atypical <EG06>
F:615-645/Domain: EGF homology <EG07>
F:652-683/Domain: EGF homology <EG08>
F:690-720/Domain: EGF homology <EG09>
F:727-796/Domain: EGF homology #status atypical <EG10>
F:803-834/Domain: EGF homology <EG11>
F:841-876/Domain: EGF homology <EG12>
F:883-914/Domain: EGF homology <EG13>
F:921-952/Domain: EGF homology <EG14>
F:997-1060/Region: cysteine-rich
F:1222-1246/Domain: transmembrane #status predicted <TML>
F:1247-1408/Domain: intracellular #status predicted <INT>
F:152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn
Query Match 27.4%; Score 1130; DB 2; Length 1408;
Best Local Similarity 33.0%; Pred. No. 1.9e-62;
Matches 226; Conservative 72; Mismatches 197; Indels 190; Gaps 16;
QY 7 LALAVVSALLCQWSSGVFELKQEFNKKGLGNRNCRCGSGPP-----CA-C 55
DB 69 LIALILLVHKISAAGNFLEILSNTNHLNGYCC---GMPAELRATKTIIGCSPC 124
QY 56 RTFPRVCLKHQY-----ASVSPPTCTYGSATVPVLGVDSFSLPD-CAGIDPAFSPNIRP 109
DB 125 TTAFLRCLKEYQTTEGASIS--TGCSFGNATKILGSSFVLSDFGVG-----AIVL 175
QY 110 PFQFTWPGTFLIIEAL---HTDSPDLDATENPERLISRLTTORHLTVGEWSQDLHSSG 166
DB 176 PFTFRWTKSFTLLIQALDMYNTSYD-----AERLIETSYSGLVLPSPWKTLDHGR 229
QY 167 RTDLRSYRPFVCDHEHYGEGSVCFRPRDDAFGHFTCGDRGERMCDPQWKGQVCTDPICL 226
DB 230 NARITVRVRVQCAVTYNTTCTTCRPRDDQFHYACGSEGGKLCINGWQGVNCEBAICK 289
QY 227 PGDDDHGVCDKGECKRGMGRVDCIRPGCVHGTCC-QPQNCQCEGWGLFCN 285
DB 290 AGCDPVHGKDRPECECPGRMGLPCNECMVYPGCKHGSCNGSAWKVCVDTNWGGILCD 349
QY 286 QDLNLYCTHKKPCRNAGTCTNTGGSY-----GDRGKM-CDPGMKQYVC-----TD 222
DB 350 QDLNFCGTHTPCKHGTCENTAPDKYRCTCAEGLSGEQCEIVEHPCATRPNRGTTCTLK 409
QY 312 -----TCSRCPYTGANCELEVECAPSKNGASCTDLESFSCTCPGFGVKVCELS 365
DB 410 TSNRTQAQVYRTSHGRSNMGRPVRRSSMRSLDHLRPEGQALNGSSSSGLVSLGSLQLOQ 469
QY 312 -----TCSRCPYTGANCELEVECAPSKNGASCTDLESFSCTCPGFGVKVCELS 365
DB 470 QLAPDFTCDCAAGWTGPTCEINIDECAGGCEPHGGTCIDLIGFRCECPPEWHGVCQVD 529
QY 366 AMTC-----ADGFCFNGGRCS 381

DB 530 VNECEAPHASAGIAANALLTTTATAIGSNLSTALLAALTSAVASTSLAIGPCINAKECR 589
QY 382 DNPDDGYTCHCPGLGSGFNCEKMDLCSGSPSCNKAACVDLGNLSYLCRCQAGPSGRYCED 441
DB 590 NQP-GSFACICKEGSGVTCENLDDC-VGQCRNGATCIDLVNDYRCACASGFTGRDCE 647
QY 442 NVDDCASSPCANGGTCRDSVNDPSTCTPGYTGKNCAPVSRCEHAPCHNGATCHQRGOR 501
DB 648 DIDECATSPCRNGGCBVWVGKFNCLICPLGYSGLCEBAKENCITPSPCLLEG-HCLNTPEG 706
QY 502 YMCECAQGYGGPNCQFLP---EPP 523
DB 707 YYCHCPPDRAGKHCEQLRLCSQPP 731
RESULT 10
A35844
Xotch protein - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C>Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
C:Accession: A35844
C:Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A:Title: Xotch, the *Xenopus* homolog of *Drosophila* notch.
A:Reference number: A35844; MUID:90385285; PMID:2402639
A:Accession: A35844
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2524 <COF>
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C:Keywords: transmembrane protein
F:146-177/Domain: EGF homology <EGX1>
F:184-215/Domain: EGF homology <EGF1>
F:222-254/Domain: EGF homology <EGF2>
F:456-487/Domain: EGF homology <EGX2>
F:757-788/Domain: EGF homology <EGF3>
F:1025-1056/Domain: EGF homology <EGX3>
F:1924-1956/Domain: ankyrin repeat homology <AN1>
F:1957-1989/Domain: ankyrin repeat homology <AN2>
F:1991-2023/Domain: ankyrin repeat homology <AN3>
F:2024-2056/Domain: ankyrin repeat homology <AN4>
F:2057-2089/Domain: ankyrin repeat homology <AN5>
Query Match 19.7%; Score 810; DB 2; Length 2524;
Best Local Similarity 31.6%; Pred. No. 2.1e-42;
Matches 184; Conservative 61; Mismatches 196; Indels 142; Gaps 21;
QY 44 CCRGSGPPCACRTFPRVCLKHQASVS---PEPPCTYGSATVPVLGVDSFSLPDGAGID 100
DB 543 CLDGPNSYTCQCTEGFTG--RHCEQDINECIPD-PCHYGTG-----KDGATF 587
QY 101 PAFSNPIRPFQFTWPGTFLIIEALHTDSPDLDATENPERLISRLTTORHLTVG----- 155
DB 588 TCLCRP-----GYTGLCDNDINECL--SKPCLNGGQCTDRENGYICTCTPKGTGVNCET 640
QY 156 --EWSQDLHSSGR-TDLRSYRPFVCDHEHYGEGSVCFRPRD-----DAFGHF 201
DB 641 KIDDCASNLCDNGKIDKIDGYECTCEPGYTGKLNININECDSPNCRNGGTCKDQINGF 700
QY 202 TC-----GDRGKM-CDPGMKQYVC-----TD 222
DB 701 TVCPDGVYDHMCLSEVNECNPNCHGACHGVNGYKCDCEAGHSGSNCDDINNECESN 760
QY 223 PTCLPQ--CDDQHG--YCDKPGCEKCRVGMQGRYC-----DECIRYPCGVHGTG----- 267
DB 761 P-CMNGGTCKDMTGAYI-----CTKAGSPGNCQTNINECSSNPCLNHGTCTDIDVAGYK 814
QY 268 -----QQPQNCQCEGWGLFCNQDLNYCT 292
DB 815 CNMCLPYTGAICAVLAPCAGSPCKNGRCKESEDEFETFCSCPPGQWQQTCEIDWNECV 874
QY 293 HHKPCRNAGTCTNTGGSYTCSRCFGYTGCANCELEVEDECAPSKNGASCTDLESFSC 352

Db 875 -NRFCRNGATQNT-NGSYKCNCKRPGYTGRCNCEMDIDDCQNPCHNGGSCSDGINMPCFN 932

Qy 353 CPPGFYKVCBELSAMTCADGCFNGGRGSDNPDGGYTCCHPLGFGNCEKMKMDLGGSSP 412

Db 933 CPAGFRGPKCEDINECASNECKNGACTCVN-SYTCQPGFSGIHCSNTTDCYESS 991

Qy 413 CSNGAKVDLNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPSTCTCPGY 472

Db 992 CFNGGTCIDGINTTCTCQPGFTGYSYQHIDNECDSPCLNGGTCQDSYGYTKCTCPGY 1051

Qy 473 TGKNKSPVSRCEHAPCHNGATCHRGORYNCECAQGVGPN 515

Db 1052 TGLNQNLRWCDSSPKNGGCKWQTNFYKCECKSGWTGYVC 1094

RESULT 11

A46019

N:Alternate names: notch protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 16-Aug-2004

C:Accession: A46019; S25144; C49175; B46438; P41569; S32109

R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid Genomics 15, 259-264, 1993

A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of A:Notch

A:Reference number: A46019; MUID:93194170; PMID:8449489

A:Status: not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-2531

A:Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:9288502; PIDN:CAA77941.1; A:Note: sequence extracted from NCBI backbone (NCBIP:127318)

R:Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; submitted to the EMBL Data Library, April 1992

A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggests A:Reference number: S25144

A:Accession: S25144

A:Molecule type: mRNA

A:Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <PRA>

A:Cross-references: EMBL:Z11886

R:Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of A:Reference number: A49175; MUID:93178563; PMID:8440332

A:Accession: C49175

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1161-1547 <LAR>

A:Cross-references: EMBL:X68278; NID:9287987; PIDN:CAA48339.1; PID:9287988

A:Experimental source: embryo

A:Note: sequence extracted from NCBI backbone (NCBIP:126159)

R:Kopan, R.; Weintraub, H.

J. Cell Biol. 121, 631-641, 1993

A:Title: Mouse notch: expression in hair follicles correlates with cell fate determination A:Reference number: A46438; MUID:93252998; PMID:8486742

A:Accession: B46438

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054

A:Experimental source: embryo

A:Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)

C:Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.

C:Comment: This protein is one of the neurogenic proteins controlling the decision between A:Genetics:

A:Gene: notch-1

A:Map position: 2

A:Note: proximal region of chromosome 2

C:Superfamily: Notch protein; ankyrin repeat homolog; EGF homolog

F:106-138/Domain: EGF homolog <EGF1>

F:144-175/Domain: EGF homolog <EGF1>

F:222-254/Domain: EGF homolog <EGF2>

F:261-292/Domain: EGF homolog <EGF2>

F:339-370/Domain: EGF homolog <EGF3>

F:416-449/Domain: EGF homolog <EGF3>

F:456-487/Domain: EGF homolog <EGF4>

F:494-525/Domain: EGF homolog <EGF5>

F:532-563/Domain: EGF homolog <EGF6>

F:607-638/Domain: EGF homolog <EGF7>

F:682-713/Domain: EGF homolog <EGF8>

F:757-788/Domain: EGF homolog <EGF9>

F:795-826/Domain: EGF homolog <EGF10>

F:873-904/Domain: EGF homolog <EGF11>

F:911-942/Domain: EGF homolog <EGF12>

F:949-980/Domain: EGF homolog <EGF13>

F:987-1018/Domain: EGF homolog <EGF14>

F:1025-1056/Domain: EGF homolog <EGF15>

F:1063-1094/Domain: EGF homolog <EGF16>

F:1149-1180/Domain: EGF homolog <EGF17>

F:1187-1218/Domain: EGF homolog <EGF18>

F:1233-1264/Domain: EGF homolog <EGF19>

F:1352-1383/Domain: EGF homolog <EGF20>

F:1391-1425/Domain: EGF homolog <EGF21>

F:1497-1528/Domain: EGF homolog <EGF22>

F:1535-1566/Domain: EGF homolog <EGF23>

F:1573-1604/Domain: EGF homolog <EGF24>

F:1611-1642/Domain: EGF homolog <EGF25>

F:1649-1680/Domain: EGF homolog <EGF26>

F:1687-1718/Domain: EGF homolog <EGF27>

F:1725-1756/Domain: EGF homolog <EGF28>

F:1763-1794/Domain: EGF homolog <EGF29>

F:1801-1832/Domain: EGF homolog <EGF30>

F:1839-1870/Domain: EGF homolog <EGF31>

F:1877-1908/Domain: EGF homolog <EGF32>

F:1915-1946/Domain: EGF homolog <EGF33>

F:1953-1984/Domain: EGF homolog <EGF34>

F:1991-2022/Domain: EGF homolog <EGF35>

F:2029-2060/Domain: EGF homolog <EGF36>

F:2067-2098/Domain: EGF homolog <EGF37>

F:2105-2136/Domain: EGF homolog <EGF38>

F:2143-2174/Domain: EGF homolog <EGF39>

F:2181-2212/Domain: EGF homolog <EGF40>

F:2219-2250/Domain: EGF homolog <EGF41>

F:2257-2288/Domain: EGF homolog <EGF42>

F:2295-2326/Domain: EGF homolog <EGF43>

F:2333-2364/Domain: EGF homolog <EGF44>

F:2371-2402/Domain: EGF homolog <EGF45>

F:2409-2440/Domain: EGF homolog <EGF46>

F:2447-2478/Domain: EGF homolog <EGF47>

F:2485-2516/Domain: EGF homolog <EGF48>

F:2523-2554/Domain: EGF homolog <EGF49>

F:2561-2592/Domain: EGF homolog <EGF50>

F:2599-2630/Domain: EGF homolog <EGF51>

F:2637-2668/Domain: EGF homolog <EGF52>

F:2675-2706/Domain: EGF homolog <EGF53>

F:2713-2744/Domain: EGF homolog <EGF54>

F:2751-2782/Domain: EGF homolog <EGF55>

F:2789-2820/Domain: EGF homolog <EGF56>

F:2827-2858/Domain: EGF homolog <EGF57>

F:2865-2896/Domain: EGF homolog <EGF58>

F:2903-2934/Domain: EGF homolog <EGF59>

F:2941-2972/Domain: EGF homolog <EGF60>

F:2979-3010/Domain: EGF homolog <EGF61>

F:3017-3048/Domain: EGF homolog <EGF62>

F:3055-3086/Domain: EGF homolog <EGF63>

F:3093-3124/Domain: EGF homolog <EGF64>

F:3131-3162/Domain: EGF homolog <EGF65>

F:3169-3200/Domain: EGF homolog <EGF66>

F:3207-3238/Domain: EGF homolog <EGF67>

F:3245-3276/Domain: EGF homolog <EGF68>

F:3283-3314/Domain: EGF homolog <EGF69>

F:3321-3352/Domain: EGF homolog <EGF70>

F:3359-3390/Domain: EGF homolog <EGF71>

F:3397-3428/Domain: EGF homolog <EGF72>

F:3435-3466/Domain: EGF homolog <EGF73>

F:3473-3504/Domain: EGF homolog <EGF74>

F:3511-3542/Domain: EGF homolog <EGF75>

F:3549-3580/Domain: EGF homolog <EGF76>

F:3587-3618/Domain: EGF homolog <EGF77>

F:3625-3656/Domain: EGF homolog <EGF78>

F:3663-3694/Domain: EGF homolog <EGF79>

F:3701-3732/Domain: EGF homolog <EGF80>

F:3739-3770/Domain: EGF homolog <EGF81>

F:3777-3808/Domain: EGF homolog <EGF82>

F:3815-3846/Domain: EGF homolog <EGF83>

F:3853-3884/Domain: EGF homolog <EGF84>

F:3891-3922/Domain: EGF homolog <EGF85>

F:3929-3960/Domain: EGF homolog <EGF86>

F:3967-3998/Domain: EGF homolog <EGF87>

F:4005-4036/Domain: EGF homolog <EGF88>

F:4043-4074/Domain: EGF homolog <EGF89>

F:4081-4112/Domain: EGF homolog <EGF90>

F:4119-4150/Domain: EGF homolog <EGF91>

F:4157-4188/Domain: EGF homolog <EGF92>

F:4195-4226/Domain: EGF homolog <EGF93>

F:4233-4264/Domain: EGF homolog <EGF94>

F:4271-4302/Domain: EGF homolog <EGF95>

F:4309-4340/Domain: EGF homolog <EGF96>

F:4347-4378/Domain: EGF homolog <EGF97>

F:4385-4416/Domain: EGF homolog <EGF98>

F:4423-4454/Domain: EGF homolog <EGF99>

F:4461-4492/Domain: EGF homolog <EGF100>

F:4499-4530/Domain: EGF homolog <EGF101>

F:4537-4568/Domain: EGF homolog <EGF102>

F:4575-4606/Domain: EGF homolog <EGF103>

F:4613-4644/Domain: EGF homolog <EGF104>

F:4651-4682/Domain: EGF homolog <EGF105>

F:4689-4720/Domain: EGF homolog <EGF106>

F:4727-4758/Domain: EGF homolog <EGF107>

F:4765-4796/Domain: EGF homolog <EGF108>

F:4803-4834/Domain: EGF homolog <EGF109>

F:4841-4872/Domain: EGF homolog <EGF110>

F:4879-4910/Domain: EGF homolog <EGF111>

F:4917-4948/Domain: EGF homolog <EGF112>

F:4955-4986/Domain: EGF homolog <EGF113>

F:4993-5024/Domain: EGF homolog <EGF114>

F:5031-5062/Domain: EGF homolog <EGF115>

F:5069-5100/Domain: EGF homolog <EGF116>

F:5107-5138/Domain: EGF homolog <EGF117>

F:5145-5176/Domain: EGF homolog <EGF118>

F:5183-5214/Domain: EGF homolog <EGF119>

F:5221-5252/Domain: EGF homolog <EGF120>

F:5259-5290/Domain: EGF homolog <EGF121>

F:5297-5328/Domain: EGF homolog <EGF122>

F:5335-5366/Domain: EGF homolog <EGF123>

F:5373-5404/Domain: EGF homolog <EGF124>

F:5411-5442/Domain: EGF homolog <EGF125>

F:5449-5480/Domain: EGF homolog <EGF126>

F:5487-5518/Domain: EGF homolog <EGF127>

F:5525-5556/Domain: EGF homolog <EGF128>

F:5563-5594/Domain: EGF homolog <EGF129>

F:5601-5632/Domain: EGF homolog <EGF130>

F:5639-5670/Domain: EGF homolog <EGF131>

F:5677-5708/Domain: EGF homolog <EGF132>

F:5715-5746/Domain: EGF homolog <EGF133>

F:5753-5784/Domain: EGF homolog <EGF134>

F:5791-5822/Domain: EGF homolog <EGF135>

F:5829-5860/Domain: EGF homolog <EGF136>

F:5867-5898/Domain: EGF homolog <EGF137>

F:5905-5936/Domain: EGF homolog <EGF138>

F:5943-5974/Domain: EGF homolog <EGF139>

F:5981-6012/Domain: EGF homolog <EGF140>

F:6019-6050/Domain: EGF homolog <EGF141>

F:6057-6088/Domain: EGF homolog <EGF142>

F:6095-6126/Domain: EGF homolog <EGF143>

F:6133-6164/Domain: EGF homolog <EGF144>

F:6171-6202/Domain: EGF homolog <EGF145>

F:6209-6240/Domain: EGF homolog <EGF146>

F:6247-6278/Domain: EGF homolog <EGF147>

F:6285-6316/Domain: EGF homolog <EGF148>

F:6323-6354/Domain: EGF homolog <EGF149>

F:6361-6392/Domain: EGF homolog <EGF150>

F:6399-6430/Domain: EGF homolog <EGF151>

F:6437-6468/Domain: EGF homolog <EGF152>

F:6475-6506/Domain: EGF homolog <EGF153>

F:6513-6544/Domain: EGF homolog <EGF154>

F:6551-6582/Domain: EGF homolog <EGF155>

F:6589-6620/Domain: EGF homolog <EGF156>

F:6627-6658/Domain: EGF homolog <EGF157>

F:6665-6696/Domain: EGF homolog <EGF158>

F:6703-6734/Domain: EGF homolog <EGF159>

F:6741-6772/Domain: EGF homolog <EGF160>

F:6779-6810/Domain: EGF homolog <EGF161>

F:6817-6848/Domain: EGF homolog <EGF162>

F:6855-6886/Domain: EGF homolog <EGF163>

F:6893-6924/Domain: EGF homolog <EGF164>

F:6931-6962/Domain: EGF homolog <EGF165>

F:6969-6999/Domain: EGF homolog <EGF166>

F:7006-7037/Domain: EGF homolog <EGF167>

F:7044-7075/Domain: EGF homolog <EGF168>

F:7082-7113/Domain: EGF homolog <EGF169>

F:7120-7151/Domain: EGF homolog <EGF170>

F:7158-7189/Domain: EGF homolog <EGF171>

F:7196-7227/Domain: EGF homolog <EGF172>

F:7234-7265/Domain: EGF homolog <EGF173>

F:7272-7303/Domain: EGF homolog <EGF174>

F:7310-7341/Domain: EGF homolog <EGF175>

F:7348-7379/Domain: EGF homolog <EGF176>

F:7385-7416/Domain: EGF homolog <EGF177>

F:7423-7454/Domain: EGF homolog <EGF178>

F:7461-7492/Domain: EGF homolog <EGF179>

F:7499-7530/Domain: EGF homolog <EGF180>

F:7537-7568/Domain: EGF homolog <EGF181>

F:7574-7605/Domain: EGF homolog <EGF182>

F:7612-7643/Domain: EGF homolog <EGF183>

F:7650-7681/Domain: EGF homolog <EGF184>

F:7687-7718/Domain: EGF homolog <EGF185>

F:7725-7756/Domain: EGF homolog <EGF186>

F:7763-7794/Domain: EGF homolog <EGF187>

F:7801-7832/Domain: EGF homolog <EGF188>

F:7839-7870/Domain: EGF homolog <EGF189>

F:7877-7908/Domain: EGF homolog <EGF190>

F:7914-7945/Domain: EGF homolog <EGF191>

F:7952-7983/Domain: EGF homolog <EGF192>

F:7990-8021/Domain: EGF homolog <EGF193>

F:8028-8059/Domain: EGF homolog <EGF194>

F:8065-8096/Domain: EGF homolog <EGF195>

F:8103-8134/Domain: EGF homolog <EGF196>

F:8141-8172/Domain: EGF homolog <EGF197>

F:8179-8210/Domain: EGF homolog <EGF198>

F:8217-8248/Domain: EGF homolog <EGF199>

F:8254-8285/Domain: EGF homolog <EGF200>

F:8292-8323/Domain: EGF homolog <EGF201>

F:8330-8361/Domain: EGF homolog <EGF202>

F:8368-8399/Domain: EGF homolog <EGF203>

F:8406-8437/Domain: EGF homolog <EGF204>

F:8444-8475/Domain: EGF homolog <EGF205>

F:8481-8512/Domain: EGF homolog <EGF206>

F:8519-8550/Domain: EGF homolog <EGF207>

F:8557-8588/Domain: EGF homolog <EGF208>

F:8595-8626/Domain: EGF homolog <EGF209>

F:8633-8664/Domain: EGF homolog <EGF210>

F:8671-8702/Domain: EGF homolog <EGF211>

F:8709-8740/Domain: EGF homolog <EGF212>

F:8747-8778/Domain: EGF homolog <EGF213>

F:8784-8815/Domain: EGF homolog <EGF214>

F:8822-8853/Domain: EGF homolog <EGF215>

F:8860-8891/Domain: EGF homolog <EGF216>

F:8898-8929/Domain: EGF homolog <EGF217>

F:8936-8967/Domain: EGF homolog <EGF218>

F:8973-9004/Domain: EGF homolog <EGF219>

F:9011-9042/Domain: EGF homolog <EGF220>

F:9049-9080/Domain: EGF homolog <EGF221>

F:9087-9118/Domain: EGF homolog <EGF222>

F:9124-9155/Domain: EGF homolog <EGF223>

F:9162-9193/Domain: EGF homolog <EGF224>

F:9200-9231/Domain: EGF homolog <EGF225>

F:9238-9269/Domain: EGF homolog <EGF226>

F:9275-9306/Domain: EGF homolog <EGF227>

F:9313-9344/Domain: EGF homolog <EGF228>

F:9351-9382/Domain: EGF homolog <EGF229>

F:9389-9420/Domain: EGF homolog <EGF230>

F:9427-9458/Domain: EGF homolog <EGF231>

F:9464-9495/Domain: EGF homolog <EGF232>

F:9502-9533/Domain: EGF homolog <EGF233>

F:9540-9571/Domain: EGF homolog <EGF234>

F:9578-9609/Domain: EGF homolog <EGF235>

F:9615-9646/Domain: EGF homolog <EGF236>

F:9653-9684/Domain: EGF homolog <EGF237>

F:9691-9722/Domain: EGF homolog <EGF238>

F:9729-9760/Domain: EGF homolog <EGF239>

F:9767-9798/Domain: EGF homolog <EGF240>

F:9804-9835/Domain: EGF homolog <EGF241>

F:9842-9873/Domain: EGF homolog <EGF242>

F:9880-9911/Domain: EGF homolog <EGF243>

F:9918-9949/Domain: EGF homolog <EGF244>

F:9956-9987/Domain: EGF homolog <EGF245>

F:9993-10000/Domain: EGF homolog <EGF246>

F:10007-10038/Domain: EGF homolog <EGF247>

F:10045-10076/Domain: EGF homolog <EGF248>

F:10083-10114/Domain: EGF homolog <EGF249>

F:10121-10152/Domain: EGF homolog <EGF250>

F:10159-10190/Domain: EGF homolog <EGF251>

F:10197-10228/Domain: EGF homolog <EGF252>

F:10235-10266/Domain: EGF homolog <EGF253>

F:10273-10304/Domain: EGF homolog <EGF254>

F:10311-10342/Domain: EGF homolog <EGF255>

F:10349-10380/Domain: EGF homolog <EGF256>

F:10387-10418/Domain: EGF homolog <EGF257>

F:10425-10456/Domain: EGF homolog <EGF258>

F:10463-10494/Domain: EGF homolog <EGF259>

F:10501-10532/Domain: EGF homolog <EGF260>

F:10539-10570/Domain: EGF homolog <EGF261>

F:10577-10608/Domain: EGF homolog <EGF262>

F:10615-10646/Domain: EGF homolog <EGF263>

F:10653-10684/Domain: EGF homolog <EGF264>

F:10691-10722/Domain: EGF homolog <EGF265>

F:10729-10760/Domain: EGF homolog <EGF266>

F:10767-10798/Domain: EGF homolog <EGF267>

F:10805-10836/Domain: EGF homolog <EGF268>

F:10843-10874/Domain: EGF homolog <EGF269>

F:10881-10912/Domain: EGF homolog <EGF270>

F:10919-10950/Domain: EGF homolog <EGF271>

F:10957-10988/Domain: EGF homolog <EGF272>

F:10995-11026/Domain: EGF homolog <EGF273>

F:11033-11064/Domain: EGF homolog <EGF274>

F:11071-11102/Domain: EGF homolog <EGF275>

F:11109-11140/Domain: EGF homolog <EGF276>

F:11147-11178/Domain: EGF homolog <EGF277>

F:11185-11216/Domain: EGF homolog <EGF278>

F:11223-11254/Domain: EGF homolog <EGF279>

F:11261-11292/Domain: EGF homolog <EGF280>

F:11299-11330/Domain: EGF homolog <EGF281>

F:11337-11368/Domain: EGF homolog <EGF282>

F:11375-11406/Domain: EGF homolog <EGF283>

F:11413-11444/Domain: EGF homolog <EGF284>

F:11451-11482/Domain: EGF homolog <EGF285>

F:11489-11520/Domain: EGF homolog <EGF286>

F:11527-11558/Domain: EGF homolog <EGF287>

F:11565-11596/Domain: EGF homolog <EGF288>

F:11603-11634/Domain: EGF homolog <EGF289>

F:11641-11672/Domain: EGF homolog <EGF290>

F:11679-11710/Domain: EGF homolog <EGF291>

F:11717-11748/Domain: EGF homolog <EGF292>

F:11755-11786/Domain: EGF homolog <EGF293>

F:11793-11824/Domain: EGF homolog <EGF294>

F:11831-11862/Domain: EGF homolog <EGF295>

F:11869-11900/Domain: EGF homolog <EGF296>

F:11907-11938/Domain: EGF homolog <EGF297>

F:11945-11976/Domain: EGF homolog <EGF298>

F:11983-12014/Domain: EGF homolog <EGF299>

F:12021-12052/Domain: EGF homolog <EGF300>

F:12059-12090/Domain: EGF homolog <EGF301>

F:12097-12128/Domain: EGF homolog <EGF302>

F:12135-12166/Domain: EGF homolog <EGF303>

F:12173-12204/Domain: EGF homolog <EGF304>

F:12211-12242/Domain: EGF homolog <EGF305>

F:12249-12280/Domain: EGF homolog <EGF306>

F:12287-12318/Domain: EGF homolog <EGF307>

F:12325-12356/Domain: EGF homolog <EGF308>

F:12363-12394/Domain: EGF homolog <EGF309>

F:12401-12432/Domain: EGF homolog <EGF310>

F:12439-12470/Domain: EGF homolog <EGF311>

F:12477-12508/Domain: EGF homolog <EGF312>

F:12515-12546/Domain: EGF homolog <EGF313>

F:12553-12584/Domain: EGF homolog <EGF314>

F:12591-12622/Domain: EGF homolog <EGF315>

F:12629-12660/Domain: EGF homolog <EGF316>

F:12667-12698/Domain: EGF homolog <EGF317>

F:12705-12736/Domain: EGF homolog <EGF318>

F:12743-12774/Domain: EGF homolog <EGF319>

F:12781-12812/Domain: EGF homolog <EGF320>

F:12819-12850/Domain: EGF homolog <EGF321>

F:12857-12888/Domain: EGF homolog <EGF322>

F:12895-12926/Domain: EGF homolog <EGF323>

F:12933-12964/Domain: EGF homolog <EGF324>

F:12971-13002/Domain: EGF homolog <EGF325>

F:13009-13040/Domain: EGF homolog <EGF326>

F:13047-13078/Domain: EGF homolog <EGF327>

F:13085-13116/Domain: EGF homolog <EGF328>

F:13123-13154/Domain: EGF homolog <EGF329>

F:13161-13192/Domain: EGF homolog <EGF330>

F:13199-13230/Domain: EGF homolog <EGF331>

F:13237-13268/Domain: EGF homolog <EGF332>

F:13275-13306/Domain: EGF homolog <EGF333>

F:13313-13344/Domain: EGF homolog <EGF334>

F:13351-13382/Domain: EGF homolog <EGF335>

F:13389-13420/Domain: EGF homolog <EGF336>

F:13427-13458/Domain: EGF homolog <EGF337>

F:13465-13496/Domain: EGF homolog <EGF338>

F:13503-1

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QY 557 LLLLGCAVVVVRLLKLOKHQPPPCGGTETETMNNLANCQREKDVSVSIIGATQIKNTN 616
Db 1130 --YCHCQAGYTSYCYDEVECSNPNP-----QNGATC-----TDYLGGSCKCV- 1172
QY 617 KKADPHDGHGAABKSSPKVRYPTVDVNLVRLDKGD-----EATVRDTH----- 658
Db 1173 --AGYHGSNCSEINECLSPQCGNGTCTIDLNTSYKSCPRGTQGVHCEINVDVDDCHPPLD 1230
QY 659 -SKRDTKC 665
Db 1231 PASRSPKC 1238

RESULT 12
S1818
notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
A:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A:Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Cross-references: EMBL:X57405; NID:957634; PID:957635
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF>
F:1233-1264/Domain: EGF homology <EGF2>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 19.3%; Score 794.5; DB 2; Length 2531;
Best Local Similarity 27.9%; Pred. No. 1.9e-41;
Matches 226; Conservative 64; Mismatches 268; Indels 253; Gaps 32;

QY 28 KLOEFVVK--KGLGN-----RNC-----CRGGS-----GPPCACRTFFRVCLKHQAS-- 69
Db 508 KNEFLCQCPKFSGLCHLCQYDVECASTPKNGAKCLDGP-----NTYTCVCTEGTGTGHC 563
QY 70 -----VSPPEPCTGSAVTPVLGVDSFSLPDGAG-----IDPAFSPNIRPFPGFTWPG 117
Db 564 EVDIDCEDPD-FCHIGLCKDGVATFTCLCPQPGVTGHHCTNINECHSQPCRHGTCQDRD 622
QY 118 TFSLLIEALHTDP-----DDLATENPERLLSRLTTQRLHVLVBWSQDLHSSGRTDLR 171
Db 623 NYLLCLCLKGTGTGPNCEINLDDCAS-NP-----CDSGTCLDKI 659
QY 172 YSYRFVCDRHYYGEGCSV-----FCRPRDDAFGHFTC----- 203
Db 660 DGYECACEPGYTGSMCNVNIDECAGSPCHNGTCTC-----EDGIAGFTCRCPGVDHPTCLSE 716
QY 204 -----GDRGERK-CDPGWKGYC-----TDPICLPG-----CDQD-QHGY 235
Db 717 VNECNSNPCHHGACRDGLNGYKCDAPGWSGTNCDINNECESNP-CVNGGCKDWTSGY 775
QY 236 CDKPECKCRVWGQRYC-----DECIRYPCVHGTCTC----- 267
Db 776 V-----CTCREGFSGPNQCTNINECASNPCLNQGTCTDIDVAGYKNCPLPYTGATCEVVL 830
QY 268 -----QQPWQNCQSGWGLFCNQDLNTCTHHKPCRNGATCTNTGQ 308
Db 831 APCATSPCKNSGVCKSESDYGSFSCVCTPGWQGTCEIDINECV-KSPCRHGASQNT-N 888
QY 309 GSYTCSRPGYTGANCELEVBDCAPSPCKNGASCITDLESFSCCTPPGYKVCBELSAMT 368
Db 889 GSYRCLCQAGYTGRCNESDIDDCRPNPCHNGSGCTDGVNAAFCDCLPGFGQAGFCEBINE 948
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QY 369 CADGCFENGRCSDNDPGYTTCHCPLGFSGFNCEKKMDLCSGSSPCSNAGKACVDLGNLYLC 428
Db 949 CATNFCQNGANCTCDV-SYTCCTPTGFGNGIHCENNTPDCTESSCFNGGTCTVDGINSFTC 1007
QY 429 RCQAGFSGRYCEBDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCASPVSRCEHAP 488
Db 1008 LCPPGFTGSYQYDVNECDSPCLHGGTCQDSYGYKCTCPQGYTGLNCQNLVRWCDSAP 1067
QY 489 CHNGATCHQQRQRYMCECAQYGGNCPQLLPE-----PPPGPMVVDLSE 533
Db 1068 CKNGGCKWQNTNTQYHCECRSGWTGFNCVLSVSCVAAAKRGIGIDVTLLCQHGLCVDEED 1127
QY 534 RHMESQGGFPFWAVCAGVLLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETETMNNL 593
Db 1128 KH-----YCHCQAGYTSYCYDEVECSNPNP-----QNG 1157
QY 594 ANCOREKDVSVSIIGATQIKNTNKKADPHDGHGAABKSSPKVRYPTVDVNLVRLDKGD--- 650
Db 1158 ATC-----TDYLGGSCKCV--AGYHGSNCSEINECLSPQCGNGTCTIDLNTWTKC 1207
QY 651 -----EATVRDTH-----SKRDTKC 665
Db 1208 SCPRGTQGVHCEINVDVDDCHPPLDPASRSPKC 1238

RESULT 13
A0136
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
N:Alternate names: epidermal growth factor homolog precursor
N:Contains: alternatively spliced fibropellin Ib (EGPI)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A40136; B40136; C40136; A29316; A43131
R:Deigadillo-Reynoso, M.G.; Rollo, D.R.; Hersh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A:Title: Structural analysis of the ueGF gene in the sea urchin Strongylocentrotus purpuratus
A:Reference number: A40136; MUID:90112459; PMID:2514273
A:Accession: A40136
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <DEL>
A:Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061
A:Accession: B40136
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
A:Accession: C40136
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'K',747-821,898-978 <DE3>
R:Hersh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A:Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A:Reference number: A29316; MUID:87319677; PMID:3498216
A:Accession: A29316
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 'S',280-481,786-1064 <HUR>
A:Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260
R:Hunt, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A:Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
A:Reference number: A43131; MUID:89196806; PMID:2784773
A:Contents: annotation
C:Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib).
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1064/Product: fibropellin I #status predicted <FIB>
F:23-54/Domain: EGF homology <EG01>
F:57-175/Domain: C1r/C1s repeat homology <C1r>
F:180-211/Domain: EGF homology <EG02>
F:218-249/Domain: EGF homology <EG03>
F:256-287/Domain: EGF homology <EG04>
F:294-325/Domain: EGF homology <EG05>
```


R.Bierkamp, C.; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A>Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern
A:Reference number: S42612; MUID:94128602; PMID:8297791
A:Accession: S42612
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2437 <BTE>
A:Cross-references: UNIPROT:P46530; EMBL:X69088; NID:G433866; PIDN:CAA48831.1; PID:G433833
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:755-786/Domain: EGF homology <EGF1>
F:1023-1054/Domain: EGF homology <EGF>
F:1185-1216/Domain: EGF homology <EGF2>
F:1915-1947/Domain: ankyrin repeat homology <AN1>
F:1948-1980/Domain: ankyrin repeat homology <AN2>
F:1982-2014/Domain: ankyrin repeat homology <AN3>
F:2015-2047/Domain: ankyrin repeat homology <AN4>
F:2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 18.6%; Score 765.5; DB 2; Length 2437;
Best Local Similarity 32.9%; Pred. No. 1.2e-39;
Matches 168; Conservative 57; Mismatches 203; Indels 82; Gaps 19;

QY 44 CRRGGSGPPCA-----CRTEFRVCLKHQASVSPEPTCYGSATVPLGVDSFSPLPDGAG 98
DB 627 CPKGTGVNCEINDDCK-----RKPCDYKGCIDKINGEYECVCEFGYSG 670
QY 99 -----IDPAFNPRIFFPGTWPGTFSLLIEALHTDPSDDLATENPERLLISRLTTQRHL 152
DB 671 SMCNINIDCALNPCHN-----GGTC-----IDGVNSFTCLCPDGFPRDATCLSQH- 715
QY 153 TVGEWSQD--LHSSGRTDLRSYRFVCDHYHGGCVS---FCRPRDDAFGHFTCGDRG 207
DB 716 ---NECSSNPCTHGSCLDQIN-SYRCVCBAGWGRNCIDIINECLSNPCNVNGG-ICKDWT 770
QY 208 EK---MCDPGWKGYC-----TDPICLPG---CDDQHGVCYDKPGECKCRVGWQRYCD 254
DB 771 SGYLCTCRAGFSGPNCOMINECASNPCLNGSCIDDVAGF-----KCNCLMLPYTGEVCE 825
QY 255 E---CIRYPCGVHGTQ---OPMQCNCEQMGGLFCNODLNVCTHKKPCRNATCTN 305
DB 826 NVLAPCSRPRCKNGGVCRESEDFQSFSCNCPAGWQGTCEVDINECVRN-PCTNGGVCTEN 884
QY 306 TQGSYTCSCREYGTGANCELEVEDCAPSPCKNGASCTDLEDSPSCTCPGPGYGVKVCELS 365
DB 885 L-RGGFQCRNPGFTGALCENDIDDCEPNPCSNNGVCQDRVNGVFVCLAGFRGERCAED 943
QY 366 AMTCADGCFNGGRCSNDPDGGYTHCPLGFSFENCEKMDLCSGSSPCSNAGKACVDLGN 425
DB 944 IDECVSAPCRNGNCTDCVN-SYTCSCPAGFSGINCEINTPDCTESSCFNGGTCVDGISS 1002
QY 426 YLCRCQAGFSGRYCDNVDVDCASSPCANGTCTCRDSVNDPFCCTCPGPGYTKNCSAPVSRCE 485
DB 1003 FSCVCLPGFTGNYQHDVNECDRSPQNGSCQDGYGTYKTCBPHGYTGLNCSQLVRWCD 1062
QY 486 HAPCHNGATCHQGRQRYMCECAQGYGGPNC 515
DB 1063 SSPCKNGSGCWQOGASFTCCQASGWTGIYC 1092

RESULT 15
A49175
Motch B protein - mouse (fragment)
N:Alternate names: Notch homolog
C:Species: Mus musculus (house mouse)
C>Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change 16-Aug-2004
C:Accession: A49175; PH1570; S32113
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A>Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A>Status: preliminary; nucleic acid sequence not shown

C:Accession: A49175; PHIS70; S32113
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Motch A and Motch B—two mouse Notch homologues coexpressed in a wide variety of
A:Reference number: A49175; PMID:93178563; PMID:8440332
A:Accession: A49175
A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-1203 <LIAR>
A:Cross-references: UNIPROT:O35516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287989
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBI:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision between
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:143-174/Domain: EGF homology <EGF1>
F:482-513/Domain: EGF homology <EGF1>
F:560-591/Domain: EGF homology <EGF>
F:674-705/Domain: EGF homology <EGF2>
F:712-743/Domain: EGF homology <EGF3>
F:836-867/Domain: EGF homology <EGX3>

Query Match 18.5%; Score 761; DB 2; Length 1203;
Best Local Similarity 32.2%; Pred. No. 1-2e-39;
Matches 186; Conservative 61; Mismatches 216; Indels 114; Gaps 21;

Qy 39 LGNNRCRGGSGPPCACRTFFRVCLKHVQASVPEPPCTYGSATPVLGVDSFSLPDGAG 98
Db 225 LNGAKCIDHFNVEYCQCATGFTGLCIDENTDNCDDPDPCHHGQCQD---GIDSYTCICNPG 281
Qy 99 -----TDPAFSNP-----IRPPFGF---TWPGTFSLIIEALHTDSDPDLATENP 139
Db 282 YMGAIQSDQIDECYSFSLNDGRCIDLVNGYQCNQPGTSGLNCEI-----NFDDCAS-NP 336
Qy 140 -----ERLIISR-----LTTQRHLTVGEBSQDLHSSGRTDLR--YSYRVCDEHYV 183
Db 337 CMHGVCVDGINRYSVCVSPGFTQRCNIDIDECASPCRKGATCINDVNGFRICPEGPH 396
Qy 184 GEGSV---FCRRPRDDAFGHFTCGDRGEK-MCDPQWKGQVC-----TDPICLPB--C 229
Db 397 HPSCYSOVNECLSNPCIHGNCCTGGLSGYKCLCDAGWGVNCEVDNRNECLSNP--CQGGTC 455
Qy 230 DD-QHGVCDDKPGCKCRVQGQRYC---DECIRYPCGVHGTG----- 267
Db 456 NNLVNGY-----RTCKKGFPGVNCQVNIDECASNPCLNQGTCTDDVSGVYTCMLPYTG 510
Qy 268 -----QQPWCNCQEGWGLFCNQDLNYCTTHHKPCRNGA 301
Db 511 KNCQTVLAPCSNPNCENAAVCKEAPNPFESFSLCAPGQWQKRCCTVDVDECI-SKPCMNNG 569
Qy 302 TCTNTGGSYTCSRPGYTGANCELEVDCECAPSPCKNGASCITLEDSPFSCCTPPGYPYKV 361
Db 570 VCHNT-QGSYVCECPGFSFGMDEEDINCLANPCQNGGSCVDHVNTFSQCCHPGFIGDK 628
Qy 362 CELSAMTCADGCFNGGRCSDNDGGVYTHCPLGFSGFENCEKMDLKGSSPCSNAGKACVD 421
Db 629 CQTDMEICLSEPCNKGTCSDSYN-SYVCTCPAGFVGHVCENNIDECTESSCFNGGTCVD 687
Qy 422 LGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAPV 481
Db 688 GINSFSLCPVPGFTGPPCLHDINECSSNPCLNAGTCVDGLGTGYRCICPLGYTGKNCQTLV 747
Qy 482 SRCEHAPCHNGATCHQGRQRYMCECAQGYGGPNQCFL 518
Db 748 NLCSRSFCKNKGTCVQEKAPHCLCPFGMDGAYCDVL 784

Search completed: November 29, 2004, 13:27:02
Job time : 22.0943 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2004, 13:12:09 ; Search time 86.9238 Seconds
(without alignments)
4779.132 Million cell updates/sec

Title: US-09-783-931-12

Perfect score: 4121

Sequence: 1 MGRSALALAWVSALLCQV.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4007	97.2	722	2	Q6PFV7	Q6pfv7 mus musculu
2	4007	97.2	722	2	AAH57400	Aah57400 mus muscu
3	4007	97.2	722	2	AAH30869	Aar30869 mus muscu
4	4007	97.2	722	2	AAH65063	Aah65063 mus muscu
5	4003	97.1	722	1	DL11_MOUSE	Q61483 mus musculu
6	3848	93.4	714	1	DL11_RAT	P97677 rattus norv
7	3652.5	88.6	723	1	DL11_HUMAN	O00548 homo sapien
8	3368	81.7	728	2	Q90656	Q90656 gallus gall
9	3167.5	76.9	721	2	Q91902	Q91902 xenopus lae
10	3146	76.3	726	2	Q8AW87	Q8aw87 cynops pyr
11	2826.5	68.6	720	2	Q8UWJ4	Q8uwj4 brachydanio
12	2823.5	68.5	717	2	P87357	P87357 brachydanio
13	2778	67.4	772	2	Q6DI48	Q6di48 brachydanio
14	2713	65.8	802	2	O57462	O57462 brachydanio
15	1902	46.2	642	2	O7ZX74	O7zxt4 xenopus lae
16	1896	46.0	642	2	P79941	P79941 xenopus lae
17	1879.5	45.6	685	1	DL14_HUMAN	Q9nr61 homo sapien
18	1832	44.5	686	1	DL14_MOUSE	Q9ji71 mus musculu
19	1828	44.4	686	2	Q9DBU9	Q9dbu9 mus musculu
20	1810.5	43.9	664	2	Q9IAT6	Q9iat6 brachydanio
21	1775.5	43.1	615	2	O57409	O57409 brachydanio
22	1630.5	39.6	684	2	Q81498	Q8i498 cupienius
23	1472	35.7	650	2	Q7Q0M5	Q7q0m5 anopheles g
24	1469.5	35.7	833	2	Q6T4M9	Q6t4m9 drosophila
25	1469.5	35.7	833	2	Q6T4N0	Q6t4n0 drosophila
26	1469.5	35.7	833	2	Q6T4N1	Q6t4n1 drosophila
27	1469.5	35.7	833	2	Q6T4N2	Q6t4n2 drosophila
28	1469.5	35.7	833	2	Q6T4N6	Q6t4n6 drosophila
29	1469.5	35.7	833	2	AAH21453	Aar21453 drosophil
30	1469.5	35.7	833	2	AAH21454	Aar21454 drosophil
31	1469.5	35.7	833	2	AAH21461	Aar21461 drosophil

32	1469.5	35.7	833	2	AAH21462	Aar21462 drosophil
33	1469.5	35.7	833	2	AAH21463	Aar21463 drosophil
34	1469.5	35.7	833	2	AAH21464	Aar21464 drosophil
35	1468.5	35.6	833	1	DL_DROME	P10041 drosophila
36	1468.5	35.6	833	2	Q6T4N3	Q6t4n3 drosophila
37	1468.5	35.6	833	2	Q6T4N4	Q6t4n4 drosophila
38	1468.5	35.6	833	2	AAO25024	AAO25024 drosophil
39	1468.5	35.6	833	2	AAH21455	Aar21455 drosophil
40	1468.5	35.6	833	2	AAH21456	Aar21456 drosophil
41	1468.5	35.6	833	2	AAH21457	Aar21457 drosophil
42	1468.5	35.6	833	2	AAH21458	Aar21458 drosophil
43	1468.5	35.6	833	2	AAH21459	Aar21459 drosophil
44	1468.5	35.6	833	2	AAH21460	Aar21460 drosophil
45	1468.5	35.6	833	2	AAH21465	Aar21465 drosophil

ALIGNMENTS

RESULT 1					
Q6PFV7	Q6PFV7	PRELIMINARY;	PRT;	722 AA.	
AC	Q6PFV7;				
DT	05-JUL-2004 (TrEMBLrel. 27, Created)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)				
DT	01-OCT-2004 (TrEMBLrel. 28, Last annotation update)				
DE	Delta-like 1.				
GN	Name=D11;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6; TISSUE=Mouse;				
RX	MEDLINE=22386257; Pubmed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RP	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6; TISSUE=Mouse;				
RA	Strausberg R.;				
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.				
RP	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6; TISSUE=Mouse;				
RA	Strausberg R.;				
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.				
RP	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J;				
RA	Nagaraja R., Waeltz P., Brathwaite M.E.;				
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.				
RP	[5]				
RP	SEQUENCE FROM N.A.				

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RC STRAIN=C57BL/6J;
RA Brachwaite M., Waeltz P., Dudekula D., Nagaraja R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; BC057400; AAH57400.1; -.
DR EMBL; BC065063; AAH65063.1; -.
DR EMBL; AY497019; AAR30869.1; -.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.
DR GO; GO:0001757; P:sonite specification of left/right symmetry; IMP.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR001174; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PR00010; EGFBLLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 97.2%; Score 4007; DB 2; Length 722;
Best Local Similarity 97.4%; Pred. No. 4.6e-269;
Matches 703; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
DB 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
QY 61 VCLKHQASVSPEPCTYGSATPVVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
DB 61 VCLKHQASVSPEPCTYGSATPVVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
QY 121 LIIEALHTSDPDLATENPERLISRLTTQRLHTLVGEWSQDLHSSGRTDLRYSYRFVCD 180
DB 121 LIIEALHTSDPDLATENPERLISRLTTQRLHTLVGEWSQDLHSSGRTDLRYSYRFVCD 180
QY 181 HYVGECSVFCRPRDDAFGHFTCGDRGERKWCDDPGWKGQYCTDPICLPGCDDOHGYCDK 240
DB 181 HYVGECSVFCRPRDDAFGHFTCGDRGERKWCDDPGWKGQYCTDPICLPGCDDOHGYCDK 240
QY 241 ECKCRVGMQGRYCDCEIRYFGVHGTCQFPWCNCOEGWGLFCNQDLNYCTHHKPCRN 300
DB 241 ECKCRVGMQGRYCDCEIRYFGVHGTCQFPWCNCOEGWGLFCNQDLNYCTHHKPCRN 300
QY 301 ATCTNTGQSGYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSPSCTCPGFGY 360
DB 301 ATCTNTGQSGYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSPSCTCPGFGY 360
QY 361 VCELSAMTCADGCFNGRCSDNPDGGYTCPLGFGSGNCKEMDLCGSSPCSNAGKCV 420
DB 361 VCELSAMTCADGCFNGRCSDNPDGGYTCPLGFGSGNCKEMDLCGSSPCSNAGKCV 420
QY 421 DLGNSYLRCQAGFGSRYCEDNVDDCASSPCANGGTCDRSDVNDFSCTCPPGYTGKNC 480
DB 421 DLGNSYLRCQAGFGSRYCEDNVDDCASSPCANGGTCDRSDVNDFSCTCPPGYTGKNC 480
QY 481 VSRCEHAPCHNGATQHQRGORYNCECAQYGGPNCOFLLPPEPPGPMVVDLSERHMSOG 540
DB 481 VSRCEHAPCHNGATQHQRGORYNCECAQYGGPNCOFLLPPEPPGPMVVDLSERHMSOG 540

QY 541 GFPPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGSETMNNLANCQREK 600
DB 541 GFPPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGSETMNNLANCQREK 600
QY 601 DVSVSIIGATQIKNTNKKADPHDGHGAESKSPKVRYPYPTVDYNLVRDLKGDEATVRDTHSK 660
DB 601 DVSVSIIGATQIKNTNKKADPHDGHGAESKSPKVRYPYPTVDYNLVRDLKGDEATVRDTHSK 660
QY 661 RDTKCSQSLOEKRRSPQHLGVGRFELTENRPSVSVSTSKDTKYQSVYVLSAEKDECVIAT 720
DB 661 RDTKCSQSLOEKRRSPQHLGVGRFELTENRPSVSVSTSKDTKYQSVYVLSAEKDECVIAT 720
QY 721 EV 722
DB 721 EV 722

RESULT 2
AAH57400 PRELIMINARY; PRT; 722 AA.
ID AAH57400;
AC AAH57400;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Delta-like 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057400; AAH57400.1; -.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 97.2%; Score 4007; DB 2; Length 722;
Best Local Similarity 97.4%; Pred. No. 4.6e-269;
Matches 703; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
DB 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCRCGGSGPPCARTTFR 60
QY 61 VCLKHQASVSPEPCTYGSATPVVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
DB 61 VCLKHQASVSPEPCTYGSATPVVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTFS 120
QY 121 LIIEALHTSDPDLATENPERLISRLTTQRLHTLVGEWSQDLHSSGRTDLRYSYRFVCD 180
DB 121 LIIEALHTSDPDLATENPERLISRLTTQRLHTLVGEWSQDLHSSGRTDLRYSYRFVCD 180
QY 181 HYVGECSVFCRPRDDAFGHFTCGDRGERKWCDDPGWKGQYCTDPICLPGCDDOHGYCDK 240
DB 181 HYVGECSVFCRPRDDAFGHFTCGDRGERKWCDDPGWKGQYCTDPICLPGCDDOHGYCDK 240
QY 241 ECKCRVGMQGRYCDCEIRYFGVHGTCQFPWCNCOEGWGLFCNQDLNYCTHHKPCRN 300
DB 241 ECKCRVGMQGRYCDCEIRYFGVHGTCQFPWCNCOEGWGLFCNQDLNYCTHHKPCRN 300
QY 301 ATCTNTGQSGYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSPSCTCPGFGY 360
DB 301 ATCTNTGQSGYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSPSCTCPGFGY 360
QY 361 VCELSAMTCADGCFNGRCSDNPDGGYTCPLGFGSGNCKEMDLCGSSPCSNAGKCV 420
DB 361 VCELSAMTCADGCFNGRCSDNPDGGYTCPLGFGSGNCKEMDLCGSSPCSNAGKCV 420
QY 421 DLGNSYLRCQAGFGSRYCEDNVDDCASSPCANGGTCDRSDVNDFSCTCPPGYTGKNC 480
DB 421 DLGNSYLRCQAGFGSRYCEDNVDDCASSPCANGGTCDRSDVNDFSCTCPPGYTGKNC 480
QY 481 VSRCEHAPCHNGATQHQRGORYNCECAQYGGPNCOFLLPPEPPGPMVVDLSERHMSOG 540
DB 481 VSRCEHAPCHNGATQHQRGORYNCECAQYGGPNCOFLLPPEPPGPMVVDLSERHMSOG 540

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Qy 121 LIIIEALHTSDSPDILATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFFVDE 180
Db 121 LIIIEALHTSDSPDILATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFFVDE 180
Qy 181 HYEGEGSVFCRPRDDAFGHFTCGDRGKMCDCPWKGOYCTDPICLPCDDOHGVCCKPG 240
Db 181 HYEGEGSVFCRPRDDAFGHFTCGDRGKMCDCPWKGOYCTDPICLPCDDOHGVCCKPG 240
Qy 241 ECKCRVGMQGRYCDCEIRYPCVHGTCCQPPQWCNCEQWGLFCNQDLNYCTHHKPCRNG 300
Db 241 ECKCRVGMQGRYCDCEIRYPCVHGTCCQPPQWCNCEQWGLFCNQDLNYCTHHKPCRNG 300
Qy 301 ATCTNTGGSYTCSCRPGYTGANCELEVDCECAPSPCKNGASCTDLESFSCCTCPGPFYVK 360
Db 301 ATCTNTGGSYTCSCRPGYTGANCELEVDCECAPSPCKNGASCTDLESFSCCTCPGPFYVK 360
Qy 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKWDLGCGSSPCSNAGKCV 420
Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKWDLGCGSSPCSNAGKCV 420
Qy 421 DLGNSYLRCQAGPSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPGTYTGKNCAP 480
Db 421 DLGNSYLRCQAGPSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPGTYTGKNCAP 480
Qy 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNQCQLLPPEPPGMVVDLSERHMSQG 540
Db 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNQCQLLPPEPPGMVVDLSERHMSQG 540
Qy 541 GPPFWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGGETETMNNLANCOREK 600
Db 541 GPPFWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGGETETMNNLANCOREK 600
Qy 601 DVSVSIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Db 601 DVSVSIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Qy 661 RDTCQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKOTKYQSVVYLSAEKDECVIAT 720
Db 661 RDTCQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKOTKYQSVVYLSAEKDECVIAT 720
Qy 721 EV 722
Db 721 EV 722

RESULT 3
AAR30869 PRELIMINARY; PRT; 722 AA.
ID AAR30869 PRELIMINARY; PRT; 722 AA.
AC AAR30869;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Delta like-1.
GN DLI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Brathwaite R., Waelitz P., Brathwaite M.E.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Brathwaite M., Waelitz P., Dudekula D., Nagaraja R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY497019; AAR30869.1;
SQ SEQUENCE 722 AA; 78449 MW; 90570B9DC7EBC75E CRC64;

Query Match 97.2%; Score 4007; DB 2; Length 722;
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Best Local Similarity 97.4%; Pred. No. 4.6e-269;
Matches 703; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
Qy 1 MGRSALALAVSALLCQVMSGVSFELKLOEFVNKKGILLGNRNCRCGSGGPPCACRTFFR 60
Db 1 MGRSALALAVSALLCQVMSGVSFELKLOEFVNKKGILLGNRNCRCGSGGPPCACRTFFR 60
Qy 61 VCLKHYSQASVPEPPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFS 120
Db 61 VCLKHYSQASVPEPPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFS 120
Qy 121 LIIEALHTSDSPDILATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFFVDE 180
Db 121 LIIEALHTSDSPDILATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFFVDE 180
Qy 181 HYEGEGSVFCRPRDDAFGHFTCGDRGKMCDCPWKGOYCTDPICLPCDDOHGVCCKPG 240
Db 181 HYEGEGSVFCRPRDDAFGHFTCGDRGKMCDCPWKGOYCTDPICLPCDDOHGVCCKPG 240
Qy 241 ECKCRVGMQGRYCDCEIRYPCVHGTCCQPPQWCNCEQWGLFCNQDLNYCTHHKPCRNG 300
Db 241 ECKCRVGMQGRYCDCEIRYPCVHGTCCQPPQWCNCEQWGLFCNQDLNYCTHHKPCRNG 300
Qy 301 ATCTNTGGSYTCSCRPGYTGANCELEVDCECAPSPCKNGASCTDLESFSCCTCPGPFYVK 360
Db 301 ATCTNTGGSYTCSCRPGYTGANCELEVDCECAPSPCKNGASCTDLESFSCCTCPGPFYVK 360
Qy 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKWDLGCGSSPCSNAGKCV 420
Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGFGFNCCKWDLGCGSSPCSNAGKCV 420
Qy 421 DLGNSYLRCQAGPSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPGTYTGKNCAP 480
Db 421 DLGNSYLRCQAGPSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPGTYTGKNCAP 480
Qy 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNQCQLLPPEPPGMVVDLSERHMSQG 540
Db 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNQCQLLPPEPPGMVVDLSERHMSQG 540
Qy 541 GPPFWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGGETETMNNLANCOREK 600
Db 541 GPPFWAVACAGVVLVLLLLGCAAVVVCVRLKQKHQPPPCGGGETETMNNLANCOREK 600
Qy 601 DVSVSIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Db 601 DVSVSIIGATQIKNTNKKADPHGDHGAESKSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660
Qy 661 RDTCQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKOTKYQSVVYLSAEKDECVIAT 720
Db 661 RDTCQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKOTKYQSVVYLSAEKDECVIAT 720
Qy 721 EV 722
Db 721 EV 722

RESULT 4
AAH65063 PRELIMINARY; PRT; 722 AA.
ID AAH65063 PRELIMINARY; PRT; 722 AA.
AC AAH65063;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Delta-like 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klauener R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065063; AAH65063.1; -
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 97.2%; Score 4007; DB 2; Length 722;
Best Local Similarity 97.4%; Pred. No. 4.6e-269;
Matches 703; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSALALAVSALLCQWSSGVFLKLOEFVFKKGLGNRCRGGSGPPCACKTFFR 60
DB 1 MGRSALALAVSALLCQWSSGVFLKLOEFVFKKGLGNRCRGGSGPPCACKTFFR 60
QY 61 VCLKHQASVPEPCTYGSANTVPLGVDSFSLPDGAGIDPAFNSPIRPFPGTWPGETS 120
DB 61 VCLKHQASVPEPCTYGSANTVPLGVDSFSLPDGAGIDPAFNSPIRPFPGTWPGETS 120
QY 121 LIIEALHTDSPDLATENPERLISRLTQRHLTVGEWSQDLHSSGRTDLRYSRFVCD 180
DB 121 LIIEALHTDSPDLATENPERLISRLTQRHLTVGEWSQDLHSSGRTDLRYSRFVCD 180
QY 181 HYGEGCSVFCPRDDAFGHFTCGDRGEXKCDPGWKGOYCTDPICLPGCDDOHGYCDK 240
DB 181 HYGEGCSVFCPRDDAFGHFTCGDRGEXKCDPGWKGOYCTDPICLPGCDDOHGYCDK 240
QY 241 ECKRCVWGQRYCDEIRYPGVGHGTCCQOPWOCNCOEGWGLFCNODLNYCTHHKPCRN 300
DB 241 ECKRCVWGQRYCDEIRYPGVGHGTCCQOPWOCNCOEGWGLFCNODLNYCTHHKPCRN 300
QY 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLSDSFCSTCPGFGY 360
DB 301 ATCTNTGQSGYTCSCRPGYTGANCELEVDCAAPSCKNGASCTDLSDSFCSTCPGFGY 360
QY 361 VCELSAMTCA DCPFCNGRCSDNPDGGYTCHPLGFSGENCEKMDLCSGSCSNGAKCV 420
DB 361 VCELSAMTCA DCPFCNGRCSDNPDGGYTCHPLGFSGENCEKMDLCSGSCSNGAKCV 420
QY 421 DLGNSVLCRCQAGFSRYCEDNVDCCASPCANGGTCRDSVNDFSCTCPGVTGKNCSP 480
DB 421 DLGNSVLCRCQAGFSRYCEDNVDCCASPCANGGTCRDSVNDFSCTCPGVTGKNCSP 480
QY 481 VSRCEHAPCHNGATCHQGRYVCECAQYGGPNCQFLPPEPPGPMVVDLSERHMSQG 540
DB 481 VSRCEHAPCHNGATCHQGRYVCECAQYGGPNCQFLPPEPPGPMVVDLSERHMSQG 540
QY 541 GPFPWAVACAGVVLVLLLLGCAAVVVCVRLKLQKHOPPEPCGGTETMNNLANCQREK 600
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QY 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSPKVRYPYPTVDYNLVRDLKGDEATVRDTHSK 660
DB 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSPKVRYPYPTVDYNLVRDLKGDEATVRDTHSK 660

601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSPKVRYPYPTVDYNLVRDLKGDEATVRDTHSK 660
661 RTKCKQSQSLQKRRSPQHLGVGRFLTENRPSVSTSTKTKYQSVYVLSAEKDECVIAT 720
661 RDTKCQSQSSAGEEIKIAPTIRGGEIPDRKRPSVSTSTKTKYQSVYVLSAEKDECVIAT 720
721 EV 722
721 EV 722

RESULT 5
DILL1 MOUSE STANDARD; PRT; 722 AA.
ID DILL1 MOUSE
AC Q61483;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
GN Name=Dill1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;
RX MEDLINE=95401858; PubMed=7671806;
RA Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
RT "Transient and restricted expression during mouse embryogenesis of
Dill1, a murine gene closely related to Drosophila Delta.";
RL Development 121:2407-2418(1995).
CC -!- FUNCTION: May be involved in cell-to-cell communication in
mammalian embryos. May have a role in cellular interactions
underlying somitogenesis and development of the nervous system.
CC -!- SUBUNIT: Interacts with Notch receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In the embryo, expressed in the paraxial
mesoderm and nervous system. Expressed at high levels in adult
heart and at lower levels, in adult lung.
CC -!- DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
CC
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X80903; CAA56865.1; -.
CC PIR; I48324; I48324.
CC HSSP; P00740; 1EDM.
CC InTract; Q61483; -.
CC MGD; MGI:104659; Dill1.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005112; F:Notch binding; IPI.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0001709; P:cell fate determination; ISS.
CC GO; GO:0007386; P:compartment specification; IMP.
CC GO; GO:0007368; P:determination of left/right symmetry; IMP.
CC GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
CC GO; GO:0009912; P:hair cell fate commitment; NAS.
CC GO; GO:0030097; P:hemopoiesis; ISS.
CC GO; GO:0042472; P:pinner ear morphogenesis; NAS.
CC GO; GO:0007399; P:neurogenesis; NAS.
CC GO; GO:0007219; P:Notch signaling pathway; ISS.
CC GO; GO:0042475; P:odontogenesis (sensu Vertebrata); NAS.
CC GO; GO:0030155; P:regulation of cell adhesion; ISS.
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DR InterPro; IPR000152; Aex_hydroxyl_s.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PS00010; EGFBLD.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 722 Delta-like protein 1.
FT DOMAIN 18 545 Extracellular (Potential).
FT TRANSMEM 546 568 Potential.
FT DOMAIN 569 722 Cytoplasmic (Potential).
FT DOMAIN 158 220 DSL.
FT DOMAIN 225 253 EGF-like 1.
FT DOMAIN 256 284 EGF-like 2.
FT DOMAIN 291 324 EGF-like 3.
FT DOMAIN 331 362 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 369 401 EGF-like 5.
FT DOMAIN 408 439 EGF-like 6.
FT DOMAIN 446 477 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 484 515 EGF-like 8.
FT DISULFID 225 236 By similarity.
FT DISULFID 229 242 By similarity.
FT DISULFID 244 253 By similarity.
FT DISULFID 256 267 By similarity.
FT DISULFID 262 273 By similarity.
FT DISULFID 275 284 By similarity.
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FT DISULFID 297 313 By similarity.
FT DISULFID 315 324 By similarity.
FT DISULFID 331 342 By similarity.
FT DISULFID 336 351 By similarity.
FT DISULFID 353 362 By similarity.
FT DISULFID 369 380 By similarity.
FT DISULFID 374 390 By similarity.
FT DISULFID 392 401 By similarity.
FT DISULFID 408 419 By similarity.
FT DISULFID 413 428 By similarity.
FT DISULFID 430 439 By similarity.
FT DISULFID 446 466 By similarity.
FT DISULFID 468 477 By similarity.
FT DISULFID 484 495 By similarity.
FT DISULFID 489 504 By similarity.
FT DISULFID 506 515 By similarity.
FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 722 AA; 78448 MW; 95F581B56DEC980 CRC64;

Query Match
Best Local Similarity 97.1%; Score 4003; DB 1; Length 722;
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGRSALALAVSALLCQWSSGVFELKQEFVNNKGLGNRNCCRGSGPPCACRFFR 60
Db 1 MGRSALALAVSALLCQWSSGVFELKQEFVNNKGLGNRNCCRGSGPPCACRFFR 60
Qy 61 VCLKHQASVSPPECTYGSATVPLGVDSFSLPDGAGIDPAFNSNIRFPFGFTWPGTFS 120
Db 61 VCLKHQASVSPPECTYGSATVPLGVDSFSLPDGAGIDPAFNSNIRFPFGFTWPGTFS 120
Qy 121 LITEALHTSDPDDLATENPERLISRLTTQRLTVGEEWSQDLHSSGRTDLRYSYRFVCD 180
Db 121 LITEALHTSDPDDLATENPERLISRLTTQRLTVGEEWSQDLHSSGRTDLRYSYRFVCD 180
Qy 181 HYTGEGCVFRCPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPTCLPGCDQHGKCPG 240

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RN (1) SEQUENCE FROM N.A.
 RP MEDLINE=99180765; PubMed=10079256;
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.,
 RT "Human ligands of the Notch receptor."
 RL Am. J. Pathol. 154:785-794 (1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Han W., Ye Q., Moore M.A.S.;
 RT "A soluble form of human delta-like-1 inhibits differentiation of
 RT hematopoietic progenitor cells."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Oda T., Chandrasekharappa S.C.;
 RT "Human Delta 1 gene sequence";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Weland D., Woods K., Xie M.-H., Yaneura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.L.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment."
 RL Genome Res. 13:2265-2270 (2003).
 RN (5)
 RP SEQUENCE FROM N.A.
 RA Almeida J.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RP FUNCTION.
 RX MEDLINE=21464863; PubMed=11581320;
 RA Jaleco A.C., Neves H., Hooiberg E., Gameiro P., Clode N., Haury M.,
 RA Henrique D., Parreira L.;
 RT "Differential effects of Notch ligands Delta-1 and Jagged-1 in human
 RT lymphoid differentiation."
 RL J. Exp. Med. 194:991-1001 (2001).
 CC -1- FUNCTION: Acts as a ligand for Notch receptors. Blocks the
 CC differentiation of progenitor cells into the B-cell lineage while
 CC promoting the emergence of a population of cells with the
 CC characteristics of a T-cell/NK-cell precursor.
 CC -1- SUBUNIT: Interacts with Notch receptors.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower
 CC expression in brain and muscle and almost no expression in
 CC placenta, lung, liver, and kidney.
 CC -1- SIMILARITY: Contains 1 DSL domain.
 CC -1- SIMILARITY: Contains 8 EGF-like domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; AF003522; AAB61286.1; -
 DR EMBL; AF196571; AAF05834.1; -
 DR EMBL; AF222310; AAG09716.1; -
 DR EMBL; AY358892; AAG89251.1; -
 DR EMBL; AL078605; CAB89569.1; -
 DR HSSP; P00740; IEDM.
 DR Genew; HGNC:2908; DLL1.

DR MIN; 606582; -
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005112; F:Notch binding; IPI.
 DR GO; GO:0030154; P:cell differentiation; TAS.
 DR GO; GO:0001709; P:cell fate determination; NAS.
 DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
 DR GO; GO:0009912; P:hair cell fate commitment; ISS.
 DR GO; GO:0030097; P:hemopoiesis; NAS.
 DR GO; GO:0042472; P:inner ear morphogenesis; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR GO; GO:0007219; P:Notch signaling pathway; NAS.
 DR GO; GO:0042475; P:odotogenesis (sensu Vertebrata); ISS.
 DR GO; GO:0030155; P:regulation of cell adhesion; TAS.
 DR InterPro; IPR000152; Aax_hydroxyl_S.
 DR InterPro; IPR001774; DSL_1.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01414; DSL; 1.
 DR Pfam; PF00008; EGF; 6.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00051; DSL; 1.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 8.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS00026; EGF_3; 7.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 723 Delta-like protein 1.
 FT DOMAIN 18 545 Extracellular (Potential).
 FT TRANSMEM 546 568 Potential.
 FT DOMAIN 569 723 Cytoplasmic (Potential).
 FT DOMAIN 159 221 DSL.
 FT DOMAIN 226 254 EGF-like 1.
 FT DOMAIN 257 285 EGF-like 2.
 FT DOMAIN 292 325 EGF-like 3.
 FT DOMAIN 332 363 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 370 402 EGF-like 5.
 FT DOMAIN 409 440 EGF-like 6.
 FT DOMAIN 447 478 EGF-like 7, calcium-binding (Potential).
 FT DOMAIN 485 516 EGF-like 8.
 FT DISULFID 226 237 By similarity.
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 FT DISULFID 409 420 By similarity.
 FT DISULFID 414 429 By similarity.
 FT DISULFID 431 440 By similarity.
 FT DISULFID 447 467 By similarity.
 FT DISULFID 469 478 By similarity.
 FT DISULFID 485 496 By similarity.
 FT DISULFID 490 505 By similarity.
 FT DISULFID 507 516 By similarity.
 FT CARBOHYD 477 477 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 498 498 E -> Q (in Ref. 2).
 FT CONFLICT 502 502 G -> R (in Ref. 4 and 5).
 FT CONFLICT 510 510 G -> S (in Ref. 2).

SQ	SEQUENCE	723 AA; 77956 MW; B4EC455FFA32A12B CRC64;	RP	SEQUENCE FROM N.A.
	Query Match	88.6%; Score 3652.5; DB 1; Length 723;	RC	TISSUE-Spinal cord;
	Best Local Similarity	86.9%; Pred. No. 1.6e-244;	RX	MEDLINE=95319507; PubMed=7596411;
	Matches 629; Conservative	46; Mismatches 46; Indels 3; Gaps 3;	RA	Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
			RT	"Expression of a Delta homologue in prospective neurons in the
			RT	chick.";
QY	1	MGRSALALAVSALLCQVSSGVFELKQEFVKNKGLGNRNCRCGGSG-PPCACRTFF 59	RL	Nature 375;787-790(1995).
DB	1	MGRSALALAVSALLCQVSSGVFELKQEFVKNKGLGNRNCRCGGAGPPCACRTFF 60	DR	EMBL; U26590; AAC59689.1; -.
			DR	PIR; I50719; I50719.
QY	60	RVCLKHQYASVPEPPCTYGSVAVTVLGVDSFSLPDGAGIDPAFNSPIRPFPGFTWPGTF 119	DR	HSSP; P00740; IEDM.
DB	61	RVCLKHQYASVPEPPCTYGSVAVTVLGVDSFSLPDGAGADSAFNSPIRPFPGFTWPGTF 120	DR	GO; GO:0016020; C:membrane; IEA.
			DR	GO; GO:0005509; F:calcium ion binding; IEA.
QY	120	SLIIIEALHTSDPDLATENPERLISRLTTORHLTVGEESQDLHSSGRTDLRYSTRFVCD 179	DR	GO; GO:0007154; P:cell communication; IEA.
DB	121	SLIIIEALHTSDPDLATENPERLISRLATQRLTVGEESQDLHSSGRTDLRYSTRFVCD 180	DR	InterPro; IPR000152; Asx_hydroxyl_S.
			DR	InterPro; IPR001774; DSL.
QY	180	EHYVGGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGOYCTDPICLPGCDQHGVCCKP 239	DR	InterPro; IPR000742; EGF 2.
DB	181	EHYVGGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGOYCTDPICLPGCDQHGVCCKP 240	DR	InterPro; IPR001881; EGF Ca.
			DR	InterPro; IPR001438; EGF II.
QY	240	GECKRVGQGRYDECIRYPGCVHGTCCQPMQCQCEGWGLFCNQDLNYCTHHKPCRN 299	DR	InterPro; IPR006209; EGF_like.
DB	241	GECKRVGQGRYDECIRYPGCVHGTCCQPMQCQCEGWGLFCNQDLNYCTHHKPCRN 300	DR	Pfam; PF01414; DSL; 1.
			DR	Pfam; PF00008; EGF; 6.
QY	300	GATCTNTGSGSYTCSRPGYGTANCLEVDPCAPSKNGASCTDLEDSCFCTCPGPGY 359	DR	PRINTS; PR00010; EGFBL00D.
DB	301	GATCTNTGSGSYTCSRPGYGTATCBLGIDECDDPSPCKNGGSCDTLENSYSTCPCPGFY 360	DR	SMART; SM00051; DSL; 1.
			DR	SMART; SM00179; EGF CA; 4.
QY	360	KVCELSAMTCAADGPCFNGRCSDNPDGGVYTCPLGFGFNCCKMDLGGSPCSNGAKC 419	DR	PROSITE; PS00010; ASX_HYDROXYL; 3.
DB	361	KICELSAMTCAADGPCFNGRCSDNPDGGVYTCPLGFGFNCCKMDLGGSPCSNGAKC 420	DR	PROSITE; PS00022; EGF_1; 8.
			DR	PROSITE; PS01186; EGF_2; 8.
QY	420	VDLGNSYLCRCQAGSGRYCENVDVDCASSPCANGGTCRDSVNDPSCFPGYTGKNCSA 479	DR	PROSITE; PS01026; EGF_3; 6.
DB	421	VDLGDAYLCRCQAGSGRHCDDNVDVDCASSPCANGGTCRDSVNDPSCFPGYTGKNCSA 480	DR	PROSITE; PS01187; EGF_CA; 2.
			KW	EGF-like domain.
QY	480	PVSRCEHAPCHNGATQHQGRYQYMECAQYGGPNCQFLLPPEPPGPMVVDLSERHMSQ 539	SQ	SEQUENCE 728 AA; 79861 MW; 93B2D6666D2388B7 CRC64;
DB	481	PVSRCEHAPCHNGATQHQGRYQYMECAQYGGPNCQFLLPPEPPGPMVVDLTER-LEQ 539		Query Match 81.7%; Score 3368; DB 2; Length 728;
				Best Local Similarity 78.5%; Pred. No. 8.3e-225;
QY	540	GGPFPMVAVCAGVILVLLLLGCAA VVVRVRLKQHPPEPCGGETMNNLANCORE 599	Matches	574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;
DB	540	GGPFPMVAVCAGVILVLLLLGCAA VVVRVRLKQHPPEPCGGETMNNLANCORE 599	QY	1
			DB	1
QY	600	KDVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYLVRLDKGDEATVRDTHS 659	QY	53
DB	600	KDVSIIIGATQIKNTNKKADFHGDHGAESKSFVRYPTVDYLVRLDKGDDTAVRDAHS 659	DB	60
			QY	112
QY	660	KRDTCQSQ-SLOEKRSPOHLGVGRFLTENRPESVYSTKTKYQSVTVLSAEKDECVI 718	DB	120
DB	660	KRDTCQSQSGSEEGKTPTTLRGGEASRRKRPDSGCSKDTKYQSVTVISEEKDECVI 719	QY	172
			DB	180
QY	719	ATEV 722	QY	232
DB	720	ATEV 723	DB	240
			QY	292
			DB	300
			QY	352
			DB	360
			QY	412
			DB	420
			QY	472
			DB	480
			QY	532
RESULT 8				
Q90656	PRELIMINARY;	PRT; 728 AA.		
AC	Q90656			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	C-Delta-1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			


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Qy 295 KPCRNGATCTNTGGSYTCSCRPYGTGANCBEVDECAPSPCKNGASCTDLEDSFSCTCP 354
Dy 294 KPCRNGATCTNTGGSYTCSCRPYGTGANCBEVDECAPSPCKNGASCTDLEDSFSCTCP 353
Qy 355 PGFYGVKVCESLMTADGCPNCGRCSDNPGGYTCHCPGLGFGPNCBKKMDLCSGSPCS 414
Dy 354 PGFYGRNCELAMTADGCPNCGHGCADNPEGGYFCQCPMGYAGFNCBKKIDHCSSNPCS 413
Qy 415 NGAKCVDLGNLYLCRCQAGFGSRYCEDNVDNDCASSPCANGGTCTRDSVNDPFCSTCPPGVTG 474
Dy 414 NDAQCLDVLVSLQCPEGFTGHCEDNIDCATYPCQNGGTGQGLSDYTCCTCPPPGVTG 473
Qy 475 KNCAPVSRCEHAPCHNGATCHORQRYWCECAGYGGPNCQFLLPEPPPPGPMVVDLSE 534
Dy 474 KNCSTAVNKLHNPCHNGATCHEMDNRYVCACIPGYGGRNCQFLLPENPQQAIVEGADK 533
Qy 535 H--MESQGGPPWAVAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGTETWNN 592
Dy 534 RYSYEEDDGGFPMTAVCAGIILVLLVLTGGSVFYIYRLKLOQRSQQID--SHSIEIETWNN 592
Qy 593 LANCO-REKDVSVIIIGATQIKNTNKKADPHGDHGAESKSPKRYPTVDYVNLVRLDKGDE 651
Dy 592 LTNNRSREKDLVSIIGATQVKNINKKVDFOSD--GDKNGFKSRYSLVDYVNLVHLEKQED 650
Qy 651 ATVRDTHSKRDTKQSQSLQEKRRSPQHL---GVGRFLTENRPSVYSTSKDTKYQSVV 708
Dy 650 LGKEDSERSEATKCEPLDSDSEKRNHLKSDSERKTE-----SLCKDTKYQSVFV 703
Qy 709 LSAEKDECVIATEV 722
Dy 704 LSEKDECVIATEI 717

RESULT 12
ID P87357 PRELIMINARY; PRT; 717 AA.
AC P87357;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Deltad transmembrane protein precursor.
GN Name=dld; Synonyms=deltad;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97346722; PubMed=9203139;
RA Dornseifer P., Takke C., Campos-Ortega J.A.;
RT "Overexpression of a zebrafish homologue of the Drosophila neurogenic
RT gene delta perturbs differentiation of primary neurons and somitic
RT development.";
RL Mech. Dev. 63:159-171(1997).
DR EMBL; Y11760; CAA72425.1; .
DR HSP; P00740; 1EDM
DR ZFIN; ZDB-GENE-990415-47; dld.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
```

```
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain; Signal; Transmembrane.
FT SIGNAL 4 11 Potential.
SQ SEQUENCE 717 AA; 95061 MW; 9C5A0162504593B4 CRC64;

Query Match 68.5%; Score 2823.5; DB 2; Length 717;
Best Local Similarity 66.3%; Pred. No. 4.1e-187;
Matches 487; Conservative 98; Mismatches 120; Indels 29; Gaps 10;

Qy 1 MGRSALALAVSALLC-----QVSSSGVFELKQEFVFNKKGKLLGNRNCRCGS--GPPCA 54
Dy 1 MGR-----LMAIVLLCWMISQGFCSGVFELKQEFVFNKKGKLVGTGNANCKGSAEAGHCE 54
Qy 55 CRTFFRVLKHQYQASVSPPEPTVGSATPVLVGVDSFSLPDGAGIDPAPSNIPFPFGFT 114
Dy 55 CKTFFRICLKHQYQANVSPDPPTVGGAVTPVLGNSPQVPESPP--DSFTNPPIPPAFGFT 113
Qy 115 WPGTFSLIIEMHTDSDDLATENPERLISRLTTQRHLTVGEESQDLHSSGRDLYSY 174
Dy 114 WPGTFSLIIEMHTDSDDLATENPERLISRLTTQRHLTVGEESQDLQVGRTELKYSY 173
Qy 175 RFVCDHYEGGCVFCRPRDDAFHFTCTDGRGEMCDPGWKGOYCTDPICLPGCDDQHG 234
Dy 174 RFVCDHYEGGCVFCRPRDDTFHFTCTGEBEIIICNSGKGOYCTEPICLPGCDEDHG 233
Qy 235 YCDKPGCKCRVGMQGRYCDCEIRYPCVHGTCCQPMQCNCQEGMGLFCNQDLYNCTHH 294
Dy 234 FCDKPGCKCRVGMQGRYCDCEIRYPCVHGTCCQPMQCNCQEGMGLFCNQDLYNCTHH 293
Qy 295 KPCNGATCTNTGGSYTCSCRPYGTGANCBEVDECAPSPCKNGASCTDLEDSFSCTCP 354
Dy 294 KPCNGATCTNTGGSYTCSCRPYGTGANCBEVDECAPSPCKNGASCTDLEDSFSCTCP 353
Qy 355 PGFYGVKVCESLMTADGCPNCGRCSDNPGGYTCHCPGLGFGPNCBKKMDLCSGSPCS 414
Dy 354 PGFYGRNCELAMTADGCPNCGHGCADNPEGGYFCQCPMGYAGFNCBKKIDHCSSNPCS 413
Qy 415 NGAKCVDLGNLYLCRCQAGFGSRYCEDNVDNDCASSPCANGGTCTRDSVNDPFCSTCPPGVTG 474
Dy 414 NDAQCLDVLVSLQCPEGFTGHCEDNIDCATYPCQNGGTGQGLSDYTCCTCPPPGVTG 473
Qy 475 KNCAPVSRCEHAPCHNGATCHORQRYWCECAGYGGPNCQFLLPEPPPPGPMVVDLSE 534
Dy 474 KNCSTAVNKLHNPCHNGATCHEMDNRYVCACIPGYGGRNCQFLLPENPQQAIVEGADK 533
Qy 535 H--MESQGGPPWAVAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGTETWNN 592
Dy 534 RYSYEEDDGGFPMTAVCAGIILVLLVLTGGSVFYIYRLKLOQRSQQID--SHSIEIETWNN 592
Qy 593 LANCO-REKDVSVIIIGATQIKNTNKKADPHGDHGAESKSPKRYPTVDYVNLVRLDKGDE 651
Dy 592 LTNNRSREKDLVSIIGATQVKNINKKVDFOSD--GDKNGFKSRYSLVDYVNLVHLEKQED 650
Qy 651 ATVRDTHSKRDTKQSQSLQEKRRSPQHL---GVGRFLTENRPSVYSTSKDTKYQSVV 708
Dy 650 LGKEDSERSEATKCEPLDSDSEKRNHLKSDSERKTE-----SLCKDTKYQSVFV 703
Qy 709 LSAEKDECVIATEV 722
Dy 704 LSEKDECVIATEV 717

RESULT 13
Q6DI48
ID Q6DI48 PRELIMINARY; PRT; 772 AA.
AC Q6DI48;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:11:34 ; Search time 60.7823 Seconds
(without alignments)
3411.281 Million cell updates/sec

Title: US-09-783-931-13

Perfect score: 3383

Sequence: 1 MGRLLASALLCVSGVFELK.....DTKYQSVYVSEKDECIATEV 578

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	73.6	740	2 AAW00876	Aaw00876 C-Delta-1
2	2485.5	73.5	727	2 AAW11719	Aaw11719 C-Delta-1
3	2483	73.4	728	3 AAY79029	Aay79029 Chick del
4	2467	72.9	722	3 AAY79028	Aay79028 Murine de
5	2466	72.9	722	2 AAW11720	Aaw11720 M-Delta-1
6	2466	72.9	722	6 ABUS55873	Abu55873 Mouse not
7	2466	72.9	722	6 AAE34029	Aae34029 Murine no
8	2401.5	71.0	723	2 AAW18353	Aaw18353 Prolifera
9	2401.5	71.0	723	2 AAW75492	Aaw75492 Human del
10	2401.5	71.0	723	2 AAW94498	Aaw94498 Human del
11	2401.5	71.0	723	3 AAY83227	Aay83227 PRO172 po
12	2401.5	71.0	723	3 AAB33422	Aab33422 Human PRO
13	2401.5	71.0	723	3 AAB24388	Aab24388 Human PRO
14	2401.5	71.0	723	3 AAY79032	Aay79032 Human del
15	2401.5	71.0	723	3 AAB00172	Aab00172 PRO172 po
16	2401.5	71.0	723	4 AAU12344	Aau12344 Human PRO
17	2401.5	71.0	723	4 AAB53064	Aab53064 Human ang
18	2401.5	71.0	723	6 ABO17788	Abol17788 Novel hum
19	2401.5	71.0	723	6 ABUS1042	Abu81042 Human PRO
20	2401.5	71.0	723	6 ABP97824	Abp97824 Amino aci
21	2401.5	71.0	723	6 ABU66742	Abu66742 Human PRO
22	2401.5	71.0	723	6 ABUS9823	Abu59823 Novel sec
23	2401.5	71.0	723	6 ABO25013	Aboc25013 Human sec
24	2401.5	71.0	723	6 ABP72566	Abp72566 Human Not
25	2401.5	71.0	723	6 ABU67018	Abu67018 Human sec

ALIGNMENTS

RESULT 1

AAW00876

ID AAW00876 standard; protein; 740 AA.

XX AAW00876;

DT 28-APR-1997 (first entry)

DE C-Delta-1 polypeptide (alternatively spliced variant).

XX C-Delta-1; cell proliferation; nervous system disorder;
KW tissue regeneration; Notch; cervix cancer; lung cancer;
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.

OS Gallus sp.

XX Key Location/Qualifiers

PH Domain 184..228

FT /label= DSL

FT Domain 229..261

FT /label= EGF1

FT Domain 262..292

FT /label= EGF2

FT Domain 293..332

FT /label= EGF3

FT Domain 333..370

FT /label= EGF4

FT Domain 371..409

FT /label= EGF5

FT Domain 410..447

FT /label= EGF6

FT Domain 448..485

FT /label= EGF7

FT Domain 486..523

FT /label= EGF8

FT Domain 524..534

FT /label= EGF9

FT Domain 555..579

FT /label= TM

FT /note= "transmembrane domain"

XX WO9701571-A1.

PN 16-JAN-1997.

PD 28-JUN-1996;

XX 96WO-US011178.

XX 28-JUN-1995;

PR 95US-0000589P.

Ada45865 Novel hum
Ada76296 Human PRO
Ada18946 Human PRO
Ada61569 Homo sapi
Adb19354 Novel hum
Adb27895 Human PRO
Ada86374 Novel hum
Ada47724 Human PRO
Ada67519 Human PRO
Adb330526 Human PRO
Ada85822 Novel hum
Ada97034 Human PRO
Ada79338 Human PRO
Ada87477 Novel hum
Adb16679 Human PRO
Ada91771 Novel hum
Adb14834 Human PRO
Adb18795 Novel hum
Ada94010 Human PRO

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA (UYVA) UNIV YALE.
XX
XX Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;
PI Gray GE;
XX
XX WPI: 1997-100159/09.
DR N-PSDB; AAT58898.
XX
XX New vertebrate Delta protein, DNA and antibodies - for treating and
PT preventing cancer, nervous system disorders and for tissue regeneration.
XX
XX Disclosure; Fig 2; 135pp; English.
XX
XX C-delta-1 polypeptide (AAW08076) is the chick homologue of Drosophila
CC Delta, a protein that binds to Notch protein. Expression of C-Delta-1
CC correlates with onset of neurogenesis. The C-delta-1 amino acid sequence
CC was deduced from a cDNA clone (AAT58898) obt'd. from chick stage 4-6
CC embryos. A shorter version (AAW58877) of C-Delta-1, lacking the 12 C-
CC terminal amino acids of the longer version, was also isolated, and mouse
CC (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have been
CC identified. Delta-1 proteins can be used to treat or prevent disorders
CC characterised by increased Notch activity, such as cervical, breast, lung
CC or colon cancer, melanoma or seminoma, and nervous system disorders or to
CC promote tissue regeneration and repair
XX
XX Sequence 740 AA;
SQ

Query Match 73.6%; Score 2489; DB 2; Length 740;
Best Local Similarity 76.0%; Pred. No. 2.9e-113;
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

QY 5 LASALIC-----VSGVFELKLOEFVNKGLLNRNCRGG-----CCTFRVCL 48
DB 11 LASALICRCQVDSGVFELKLOEFVNKGLLNRNCRGGGPGAGQQCCKTFRVCL 70
QY 49 KHYQASVPEPCTYCSA-TPVLG--SFS-PCGAG--DPAFNPFRFGFTWPGTFSLI 102
DB 71 KHYQASVPEPCTYCSAITPVLGANSFVPGAGGADPAFNPFRFGFTWPGTFSLI 130
QY 103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEMSQDLHSSGRTDL-YSYRFVCDHY 158
DB 131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEMSQDLHSSGRTDLKYSYRFVCDHY 190
QY 159 YEGGCSVFCRPRDD-FGHTCG-RGK-C-PGWKGQYCT-PICLPCDD-QHG-CDKPGBC 211
DB 191 YEGGCSVFCRPRDDRFGHFTCGERGKVCNPGWKQGYCTEPICLPGCDEHGFCDKPGBC 250
QY 212 KCRVGMQGRYCDRCIRPGCVHGTCCQPMQCNQCEGMGLFCNQDLNYCTHHKPC-NGAT 270
DB 251 KCRVGMQGRYCDRCIRPGCVHGTCCQPMQCNQCEGMGLFCNQDLNYCTHHKPCNGAT 310
QY 271 CNTNGGSYTCSCRPGYTG--CE--EEC--PCKN-GSCTDLES--SCTCPPGFYK-C 318
DB 311 CNTNGGSYTCSCRPGYTGSSCIEINECDANPCKNCGSCTDLENSYSTCPCPGFYKNC 370
QY 319 ELSAMTCADGPCPNRGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
DB 371 ELSAMTCADGPCPNRGRC-DNPDGGY-C-CPLG-SGFNCEKKIDYCSSPCANGAQCVDL 430
QY 370 GNSY-C-COAGF-GR-C-DNVDDCAS-PC-NGTCD--VND-SCTCPGY-GKNC-PVS 417
DB 431 GNSYICQCAQFGRHCDNDVDCASFPVPCVQDGVNDYSTCPCPGYNGKNCSTPVS 490
QY 418 RCEH-PCNHGATCHRR---YCECA-GYGG-NQFLLPEPP-GPV-----DEQ 458
DB 491 RCEHPCNHGATCHERSNRYVCECARGYGLNCQFLPPEPQGPVVDTEKYTEGQNSQ 550
QY 459 FPA-AVCAGLVL---LLGCAA-VVCRVLK-----QKPEC---ETTMNLANCOREKD- 504
DB 551 FPAIVACAGLILVLLGCAAIVVCRVLKVRHHRHQPEACRSETETMNNLANCOREKDI 610

QY 505 --SSIGATQIKNTKK-DFFH-----DK--KVRYP-VDYNLVLKV-----HKKC--- 541
DB 611 SISVIGATQIKNTKKVDFHSDNSDKNGYKVRYPVDYNLVLKVEDSVKKEHGKCEAK 670
QY 542 -----SEKAL-----RKRP-SVYSTSKDTKYQSYV--SEKDEC-IATEV 578
DB 671 CETYDSEAEKSAVOLKSSDTSERKRPSVYSTSKDTKYQSYVVISEKDECIATEV 728

RESULT 2
AAW11719
ID AAW11719 standard; protein; 727 AA.
XX
AC AAW11719;
XX
DT 28-APR-1997 (first entry)
XX
DE C-Delta-1 polypeptide.
XX
KW C-Delta-1; cell proliferation; nervous system disorder;
KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Domain 184..228
FT /label= DSL
FT Domain 229..261
FT /label= EGF1
FT Domain 262..292
FT /label= EGF2
FT Domain 293..332
FT /label= EGF3
FT Domain 333..370
FT /label= EGF4
FT Domain 371..409
FT /label= EGF5
FT Domain 410..447
FT /label= EGF6
FT Domain 448..485
FT /label= EGF7
FT Domain 486..523
FT /label= EGF8
FT Domain 524..534
FT /label= EGF9
FT Domain 555..579
FT /label= TM
FT /note= "transmembrane domain"
XX
XX WO9701571-A1.
XX
XX 16-JAN-1997.
XX
XX 28-JUN-1996; 96WO-US011178.
XX
XX 28-JUN-1995; 95US-0000589P.
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX (UYVA) UNIV YALE.
XX
XX Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;
XX Gray GE;
XX
XX WPI: 1997-100159/09.
XX N-PSDB; AAT58897.
XX
XX New vertebrate Delta protein, DNA and antibodies - for treating and
XX preventing cancer, nervous system disorders and for tissue regeneration.
XX
XX Disclosure; Fig 2; 135pp; English.
XX
XX C-delta-1 polypeptide (AAW11719) is the chick homologue of Drosophila

CC Delta, a protein that binds to Notch protein. Expression of C-Delta-1
 CC correlates with onset of neurogenesis. The C-delta-1 amino acid sequence
 CC was deduced from a cDNA clone (AAT5897) obtd. from chick stage 4-6
 CC embryos. An alternatively spliced variant (AAW00876) was also isolated,
 CC and mouse (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have
 CC been identified. Delta-1 proteins can be used to treat or prevent
 CC disorders characterised by increased Notch activity, such as cervical,
 CC breast, lung or colon cancer, melanoma or seminoma, and nervous system
 CC disorders or to promote tissue regeneration and repair
 CC
 SQ Sequence 727 AA;

Query Match 73.5%; Score 2485.5; DB 2; Length 727;
 Best Local Similarity 76.0%; Pred. No. 4.2e-113;
 Matches 545; Conservative 10; Mismatches 19; Indels 143; Gaps 65;

QY 5 LASALLC-----VSGVFELKLOEFVNKKGLL-NRNCRRGG-----CCTFFRVCL 48
 DB 11 LLSALLCRCQVDSGVFELKLOEFVNKKGLLSNRNCRGCGGGAGGQOQCDCKTFFRVCL 70

QY 49 KHYQASVSPPTCTYGS-TPVLG--SFS-PDGAG--DPAFSNIRPFPGFTWPTGTSLI 102
 DB 71 KHYQASVSPPTCTYGS-TPVLG--SFS-PDGAG--DPAFSNIRPFPGFTWPTGTSLI 130

QY 103 IEALHTDSPDL-TENPERLSRL-TQRLH-VGEWSDQLHSSGRTDL-YSYRFVCDHY 158
 DB 131 IEALHTDSPDL-TENPERLSRL-TQRLH-VGEWSDQLHSSGRTDL-KYSYRFVCDHY 190

QY 159 YGEGCSVFCRRDP-FGHTCG-RGEK-C-PGWGOYCT-PICLPQCD-QHG-COKPGEC 211
 DB 191 YGEGCSVFCRRDP-FGHTCG-RGEK-C-PGWGOYCT-PICLPQCD-QHG-COKPGEC 250

QY 212 KCRVGMQRYCDEIRYPGVGHGTQCPWQCNCEGWLFCNDLNYCTHHPK-NGAT 270
 DB 251 KCRVGMQRYCDEIRYPGVGHGTQCPWQCNCEGWLFCNDLNYCTHHPK-NGAT 310

QY 271 CTNTGQGSYTCSPRGYTG--CE---BEC---PCKN-GSCDTLES---SCTCPPGFYGK-C 318
 DB 311 CTNTGQGSYTCSPRGYTG--CE---BEC---PCKN-GSCDTLES---SCTCPPGFYGK-C 370

QY 319 ELSAMTCADGFCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
 DB 371 ELSAMTCADGFCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 430

QY 370 GNSY-C-COAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPGPGY-GKNC-PVS 417
 DB 431 GNSY-C-COAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPGPGY-GKNC-PVS 490

QY 418 RCEH-PCNHGATCHRR-----YCECA-GYGG-NCQFLPPEP-GPV-----DEEQ 458
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 DB 551 FPWAVCAGILVLLMLLGCAGAAVIVVVRLLVQKREKQPEACRSTETNNLANCOREKD 610

QY 505 -SSIGATQIKNTKK-DPH---DK---KVRYP-VDNVNLVKV-----HKCK---- 541
 DB 611 ISVIGATQIKNTKKVDFHSDNSDNKGVKRYPSVDNLVHLEKNSVKEEKGKCAK 670

QY 542 -----SEKAL-----RKRP-SVYSTSKDTKYQSYV--SEKDEC-IATEV 578
 DB 671 EYDSEAEKSAVLKSSDTSERKRPDSVYSTSKDTKYQSYVVISEKDECIATEV 727

RESULT 3
 AAY79029
 ID AAY79029 standard; protein; 728 AA.
 XX
 AC AAY79029;
 XX
 DT 06-JUN-2000 (first entry)
 XX

DE Chick delta protein amino acid sequence.
 XX Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;
 KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;
 KW tissue regeneration; liver cirrhosis; keloid formation; baldness;
 KW inner ear disorder; chick.
 OS Gallus sp.
 XX WO200002897-A2.
 XX 20-JAN-2000.
 XX 13-JUL-1999; 99WO-US015817.
 PR 13-JUL-1998; 98US-0092513P.
 PR 19-OCT-1998; 98US-0104834P.
 XX (UYUA) UNIV YALE.
 XX Artavanis-Teakonas S, Rand MD, Qi H;
 DR WPI; 2000-282852/24.
 XX New cleavage peptide, nucleic acids and antibodies useful for diagnosis,
 XX prevention and treatment of cancer, disorders of central nervous system,
 XX cirrhosis and psoriasis.
 PS Claim 1; Fig 3; 177pp; English.
 XX This sequence represents the chick delta protein amino acid sequence.
 CC Delta is a topothymic protein that contains a sequence which is cleaved
 CC by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz
 CC results in two fragments, a soluble amino terminal fragment consisting
 CC essentially of the extracellular domain, and a membrane bound fragment
 CC consisting of the transmembrane domain and the intracellular domain. The
 CC soluble fragment is able to bind to Notch. Delta plays a key role in
 CC differentiation, and therefore detection and measurement of delta
 CC activation is important in the study of differentiation. The invention
 CC relates to the delta cleavage peptides (the active fragment), and to
 CC methods for detecting and measuring delta activation. Delta cleavage
 CC peptides, and chimeric proteins are useful for modulating the activity of
 CC Notch, delta or kuz or at least one of the signalling pathways in a cell
 CC or organism, expressing Notch. By contacting a cell with kuz protein or
 CC nucleic acid or its antibody, the activity or levels of delta protein is
 CC modulated and vice versa. A delta cleavage peptide or its derivative
 CC capable of binding kuz protein is useful for treating or preventing a
 CC disease or disorder associated with increased delta activity or
 CC expression such as cervical, breast, colon or lung cancer, melanoma or
 CC seminoma in humans. A recombinant cell comprising a delta peptide is
 CC useful for treating or preventing central nervous system disorders. A
 CC delta cleavage peptide is useful for the diagnosis of diseases or
 CC disorders associated with increased levels of Notch-delta protein binding
 CC activity comprising measuring the ability of delta cleavage peptides in a
 CC sample to bind kuz protein. A complex of delta protein and kuz is useful
 CC for diagnosing or screening for the presence of, or predisposition to
 CC developing a disease or disorder associated with aberrant levels of the
 CC complex, comprising measuring the level or functional activity of the
 CC complex or RNA encoding delta or kuz in a sample. The delta cleavage
 CC peptide is also useful for promoting tissue regeneration and repair, for
 CC treating liver cirrhosis, keloid formation, psoriasis, baldness and
 CC degenerative or traumatic disorders of the sensory epithelium of the
 CC inner ear
 XX

Query Match 73.4%; Score 2483; DB 3; Length 728;
 Best Local Similarity 75.9%; Pred. No. 5.6e-113;
 Matches 545; Conservative 9; Mismatches 20; Indels 144; Gaps 65;

QY 5 LASALLC-----VSGVFELKLOEFVNKKGLL-NRNCRRGG-----GCTTFFRVCL 48
 DB 11 LLSALLCRCQVDSGVFELKLOEFVNKKGLLSNRNCRGCGGGAGGQOQCDCKTFFRVCL 70

QY 49 KHYQASVSEPPCTYGS-TPVLG--SFS-PDGAG--DPAFNPPIRPFPGFTWPGTFSLI 102
 DB 71 KHYQASVSEPPCTYGSATIPVLGANSFVDPGAGGAPAFNPPIRPFPGFTWPGTFSLI 130
 QY 103 IEALHTDSDDLL--TENPERLISRL--TORHL--VGEEMSQLHSSGRDLDL--YSYRFVCDHEY 158
 DB 131 IEALHTDSDDLL--TENPERLISRL--TORHL--VGEEMSQLHSSGRDLDL--YSYRFVCDHEY 190
 QY 159 YGEGSVFCRPRDD--FGHTFCG--RGEK--C--PGWKQGYCT--PICLPDGD--QHG--CDKPGBC 211
 DB 191 YGEGSVFCRPRDD--FGHTFCG--RGEK--C--PGWKQGYCT--PICLPDGD--QHG--CDKPGBC 250
 QY 212 KCRVGMQGRYCDCEIRYPCGVHCTCOOPWQCNQCEGGLFCNODLNYCTHKKPC--NGAT 270
 DB 251 KCRVGMQGRYCDCEIRYPCGVHCTCOOPWQCNQCEGGLFCNODLNYCTHKKPC--NGAT 310
 QY 271 CNTNGGYSYTCRPGYTG--CE--EEC--PCKN--GSCDTLES--SCTCPPGFYGK--C 318
 DB 311 CNTNGGYSYTCRPGYTG--CE--EEC--PCKN--GSCDTLES--SCTCPPGFYGK--C 370
 QY 319 ELSAMTCADGCPFNQGR--DNDPGY--C--CPLG--SGFNCEKK--DCSSPC--NGA--CVDL 369
 DB 371 ELSAMTCADGCPFNQGR--DNDPGY--C--CPLG--SGFNCEKK--DCSSPC--NGA--CVDL 430
 QY 370 GNSY--C--COAGF--GR--C--DNVDDCAS--PC--NGGTC--VND--SCTCPPGY--GNKCS--PVS 417
 DB 431 GNSY--C--COAGF--GR--C--DNVDDCAS--PC--NGGTC--VND--SCTCPPGY--GNKCS--PVS 490
 QY 418 RCEH--PCHNGATCHRR--YCECA--GYGG--NQFLLPPEP--GPV--DEBQ 458
 DB 491 RCEH--PCHNGATCHRR--YCECA--GYGG--NQFLLPPEP--GPV--DEBQ 550
 QY 459 FPM--AVCAGLVL--LLGCAA--VVCRLK--QKPEC--ETETMNNLANCQREKD--504
 DB 551 FPM--AVCAGLVL--LLGCAA--VVCRLK--QKPEC--ETETMNNLANCQREKD--510
 QY 505 --SSIGATQIKNTKK--DFH--DK--KVRYP--VDYNLVLKV--HKKC--541
 DB 611 SISVIGATQIKNTKK--DFH--DK--KVRYP--VDYNLVLKV--HKKC--541
 QY 542 -----SBEKAL-----RKRP--SVYSTSKDTKYQSVV--SEKDEC--IATEV 578
 DB 671 CETYDSEAEKSAVLKSSDTSERKPDVSYSTSKDTKYQSVVISEEKDECIATEV 728

RESULT 4

AAAY79028
 ID AAAY79028 standard; protein; 722 AA.

AC AAAY79028;

DT 06-JUN-2000 (first entry)

DE Murine delta protein amino acid sequence.

DE Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;
 KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;
 KW tissue regeneration; liver cirrhosis; keloid formation; baldness;
 KW inner ear disorder; mouse.

OS Mus sp.

PN WO200002897-A2.

XX 20-JAN-2000.

XX 13-JUL-1999; 99WO-US015817.

XX 13-JUL-1998; 98US-0092513P.

PR 19-OCT-1998; 98US-0104834P.

XX (UYVA) UNIV YALE.

XX Artavanis-Tsakonas S, Rand MD, Qi H;
 XX WPI; 2000-282852/24.
 XX New cleavage peptide, nucleic acids and antibodies useful for diagnosis,
 PT prevention and treatment of cancer, disorders of central nervous system,
 PT cirrhosis and psoriasis.
 XX Claim 1; Fig 3; 177pp; English.

XX This sequence represents the murine delta protein amino acid sequence.
 CC Delta is a topothymic protein that contains a sequence which is cleaved
 CC by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz
 CC results in two fragments, a soluble amino terminal fragment consisting
 CC essentially of the extracellular domain, and a membrane bound fragment
 CC consisting of the transmembrane domain and the intracellular domain. The
 CC soluble fragment is able to bind to Notch. Delta plays a key role in
 CC differentiation, and therefore detection and measurement of delta
 CC activation is important in the study of differentiation. The invention
 CC relates to the delta cleavage peptides (the active fragment), and to
 CC methods for detecting and measuring delta activation. Delta cleavage
 CC peptides, and chimeric proteins are useful for modulating the activity of
 CC Notch, delta or kuz or at least one of the signalling pathways in a cell
 CC or organism, expressing Notch. By contacting a cell with kuz protein or
 CC nucleic acid or its antibody, the activity or levels of delta protein is
 CC modulated and vice versa. A delta cleavage peptide or its derivative
 CC capable of binding kuz protein is useful for treating or preventing a
 CC disease or disorder associated with increased delta activity or
 CC expression such as cervical, breast, colon or lung cancer, melanoma or
 CC seminoma in humans. A recombinant cell comprising a delta peptide is
 CC useful for treating or preventing central nervous system disorders. A
 CC delta cleavage peptide is useful for the diagnosis of diseases or
 CC disorders associated with increased levels of Notch-delta protein binding
 CC activity comprising measuring the ability of delta cleavage peptides in a
 CC sample to bind kuz protein. A complex of delta protein and kuz is useful
 CC for diagnosing or screening for the presence of, or predisposition to
 CC developing a disease or disorder associated with aberrant levels of the
 CC complex, comprising measuring the level or functional activity of the
 CC complex or RNA encoding delta or kuz in a sample. The delta cleavage
 CC peptide is also useful for promoting tissue regeneration and repair, for
 CC treating liver cirrhosis, keloid formation, psoriasis, baldness and
 CC degenerative or traumatic disorders of the sensory epithelium of the
 CC inner ear

XX Sequence 722 AA;

Query Match 72.9%; Score 2467; DB 3; Length 722;
 Best Local Similarity 76.6%; Pred. No. 3.3e-112;
 Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;
 QY 1 MGR-----LLASALLC---VSGVFELKLQEPVKKGLL--NRNCCRGG-----GCCTFFR 45
 DB 1 MGRSALALAVVSALLCQVWCVSGVFELKLQEPVKKGLLGNRNCRCGGSGPPCACKTFFR 60
 QY 46 VCLKHQASVSEPPCTYGS-TPVLG--SFS-PDGAG--DPAFNPPIRPFPGFTWPGTFS 100
 DB 61 VCLKHQASVSEPPCTYGSATIPVLGANSFVDPGAGGAPAFNPPIRPFPGFTWPGTFS 120
 QY 101 IEALHTDSDDLL--TENPERLISRL--TORHL--VGEEMSQLHSSGRDLDL--YSYRFVCD 156
 DB 121 IEALHTDSDDLL--TENPERLISRL--TORHL--VGEEMSQLHSSGRDLDL--YSYRFVCD 180
 QY 157 HYGEGSVFCRPRDD--FGHTFCG--RGEK--C--PGWKQGYCT--PICLPDGD--QHG--CDKPG 209
 DB 181 HYGEGSVFCRPRDD--FGHTFCG--RGEK--C--PGWKQGYCT--PICLPDGD--QHG--CDKPG 240
 QY 210 ECKCRVGMQGRYCDCEIRYPCGVHCTCOOPWQCNQCEGGLFCNODLNYCTHKKPC--NG 268
 DB 241 ECKCRVGMQGRYCDCEIRYPCGVHCTCOOPWQCNQCEGGLFCNODLNYCTHKKPC--NG 300
 QY 269 ATCTNTGGSYTCRPGYTG--CE--EEC--PCKN--GSCDTLES--SCTCPPGFYGK 317
 DB 269 ATCTNTGGSYTCRPGYTG--CE--EEC--PCKN--GSCDTLES--SCTCPPGFYGK 317

Db 301 ATCTNTGGSVTCSCRPYGTGANCELEVEBCDPSCKNGASCTDLEQSFSTCTCPGFGYK 360
 Qy 318 -CELSAMTCADGPCFNGGRC-DNPDGG-YC-CPLG-SGFNCEKDD--C-SSPC-NGA-CV 367
 Db 361 VCELSAMTCADGPCFNGGRCSDNPDGGYCCPLGSGFNCEKDDKMDLCSGSPCSNGAKCV 420
 Qy 368 DLGNSY-C-COAGF-GR-C-DNVDCA-SPC-NGGTC--DVND-SCTCPGY-GKNC-S-P 415
 Db 421 DLGNSYLCRCQAGFSGRYCFDNVDCCASSPCANGGTCRDSVNDPSCTCPGYTGKNCAP 480
 Qy 416 VSRCEH-PCNHGATCHRR---YCECA-GYGG-NCQELLPE-PPGP--VD-----REQ- 458
 Db 481 VSRCEHAPCHGATCHRGQRYMCECAQYGGNQCQLLPPPPGPMVVDLSERHMSQ 540
 Qy 459 --FPW-AVCAGLV---LILLGCAA-VVCLRLK-QK---PE-C--ETETMNNLANCQREK 503
 Db 541 GPPFWAVACAGVLVLLLLGCAA-VVCLRLKQKHQPPPPGCGGETETMNNLANCQREK 600
 Qy 504 D---SSIGATOIKNTNKK-DPHDK-----KVRYP-VDYNLV--LK-----VHKK 540
 Db 601 DVSVSIIGATQIKNTNKKADPHGDKAKSKSFVRYPTVDYNLVRLDLKGDATVRDTHSK 660
 Qy 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IAT 576
 Db 661 RDTKQSQSSAGEEKIAPTIRGGEIPDRKRPESVYSTSKDTKYQSVVLSAEKDECVIAT 720
 Qy 577 EV 578
 Db 721 EV 722

RESULT 5
 ID AAW11720 standard; protein; 722 AA.
 AC AAW11720;
 XX
 XX
 DT 28-APR-1997 (first entry)
 XX
 DE M-Delta-1 polypeptide.
 XX
 KW M-Delta-1; cell proliferation; nervous system disorder;
 KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;
 KW colon cancer; melanoma; seminoma; neurogenesis; therapy.
 XX
 OS Mus sp.
 XX
 PN WO9701571-A1.
 XX
 PD 16-JAN-1997.
 XX
 PF 28-JUN-1996; 96WO-US011178.
 XX
 PR 28-JUN-1995; 95US-0000589P.
 XX
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA (UYVA) UNIV YALE.
 XX
 XX Ish-Horowitz D, Henrique D, Lewis J, Artavanis-Teakonas S;
 PI Gray GE;
 XX
 XX WPI; 1997-100159/09.
 DR N-PSDB; AAT58899.
 XX
 XX New vertebrate Delta protein, DNA and antibodies - for treating and
 PT preventing cancer, nervous system disorders and for tissue regeneration.
 PS
 PS Claim 4; Fig 8; 135pp; English.
 XX
 CC M-Delta-1 polypeptide (AAW11720) is the mouse homologue of Drosophila
 CC Delta, a protein that binds to Notch protein. It is expressed primarily
 CC in presomitic mesoderm, the central and peripheral nervous systems, and
 CC kidney. Chick (AAW11719) and human (AAW11721-38) Delta-1 polypeptides

CC have also been identified. Delta-1 proteins can be used to treat or
 CC prevent disorders characterised by increased Notch activity, such as
 CC cervical, breast, lung or colon cancer, melanoma or seminoma, as well as
 CC nervous system disorders, and to promote tissue regeneration and repair
 XX
 SQ Sequence 722 AA;
 Query Match 72.9%; Score 2466; DB 2; Length 722;
 Best Local Similarity 76.6%; Pred. No. 3,7e-112;
 Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;
 Qy 1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRCRG-----GCCTFFR 45
 Db 1 MGRSALALAVSALLCQVMSSGVFELKQEFVNKKGLLGNRNCRCGSGPPACRTFFR 60
 Qy 46 VCLKHQYQASVSPPPCTYGA-TPVLG--SFS-PDGAG-DPAFNPTRFPFGFTWPGTFS 100
 Db 61 VCLKHQYQASVSPPPCTYGSATPVLGVDVSFSPDGAGIDPAFNPTRFPFGFTWPGTFS 120
 Qy 101 LIIEALHTDSPDDL-TENPERLISRL--TORHL-VGEEMSQDLHSSGRDIL-VSYRPFVCD 156
 Db 121 LIIEALHTDSPDDLATENPERLISRLTORHLTVGEEMSQDLHSSGRDILVSYRPFVCD 180
 Qy 157 HYYGEGSVFCRRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209
 Db 181 HYYGEGSVFCRRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGDDQHGCDKPG 240
 Qy 210 ECKRVGMQGRYCDCEIRYPCVHGTCQOPWQNCQEGGGLFCNODLNTCTHHKPC-NG 268
 Db 241 ECKRVGMQGRYCDCEIRYPCGLHGTQQPQWQNCQEGGGLFCNODLNTCTHHKPCRN 300
 Qy 269 ATCTNTGGSVTCSCRPYGTG---CE---EBC---PCKNG-SCTDLES--SCTCPGFGYK 317
 Db 301 ATCTNTGGSVTCSCRPYGTGANCELEVEBCAPCKNGASCTDLESFSTCTCPGFGYK 360
 Qy 318 -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKDD--C-SSPC-NGA-CV 367
 Db 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCPLGSGFNCEKDDKMDLCSGSPCSNGAKCV 420
 Qy 368 DLGNSY-C-COAGF-GR-C-DNVDCA-SPC-NGGTC--DVND-SCTCPGY-GKNC-S-P 415
 Db 421 DLGNSYLCRCQAGFSGRYCEDNVDCCASSPCANGGTCRDSVNDPSCTCPGYTGKNCAP 480
 Qy 416 VSRCEH-PCNHGATCHRR---YCECA-GYGG-NCQELLPE-PPGP--VD-----REQ- 458
 Db 481 VSRCEHAPCHGATCHRGQRYMCECAQYGGNQCQLLPPPPGPMVVDLSERHMSQ 540
 Qy 459 --FPW-AVCAGLV---LILLGCAA-VVCLRLK-QK---PE-C--ETETMNNLANCQREK 503
 Db 541 GPPFWAVACAGVLVLLLLGCAA-VVCLRLKQKHQPPPPGCGGETETMNNLANCQREK 600
 Qy 504 D---SSIGATOIKNTNKK-DPHDK-----KVRYP-VDYNLV--LK-----VHKK 540
 Db 601 DVSVSIIGATQIKNTNKKADPHGDKAKSKSFVRYPTVDYNLVRLDLKGDATVRDTHSK 660
 Qy 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IAT 576
 Db 661 RDTKQSQSSAGEEKIAPTIRGGEIPDRKRPESVYSTSKDTKYQSVVLSAEKDECVIAT 720
 Qy 577 EV 578
 Db 721 EV 722
 RESULT 6
 ABU55873
 ID ABU55873 standard; protein; 722 AA.
 XX
 AC ABU55873;
 XX
 DT 25-MAR-2003 (first entry)
 XX
 DE Mouse notch ligand delta-like 1 protein.

XX Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation;
 KW ligand; Parkinson's disease; Huntington's disease; motor neuron disease;
 KW heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS;
 KW acquired immunodeficiency syndrome.
 XX Mus sp.
 OS WO200277204-A2.
 PN 03-OCT-2002.
 PD 25-MAR-2002; 2002WO-GB001195.
 PP 23-MAR-2001; 2001GB-00007296.
 PR 23-MAR-2001; 2001GB-00007299.
 PR 17-APR-2001; 2001GB-00009346.
 XX (AXOR-) AXORDIA LTD.
 PA Andrews P, Walsh J, Gokhale P;
 PI WPI; 2003-092852/08.
 DR N-PSDB; ABX75296.
 XX Modulating the differentiation of embryonic stem cells by providing
 PT ligands which bind receptors in the Notch and Wnt pathways, useful for
 PT treating diseases such as Parkinson's, Huntington's, heart disease,
 PT diabetes and AIDS.
 XX Claim 6; Fig 3; 121pp; English.
 PS The invention relates to modulating the differentiation of an embryonic
 CC stem cell, comprising: (a) providing a culture of embryonic stem cells;
 CC (b) providing at least one ligand or its active binding fragment, capable
 CC of binding its cognate receptor polypeptide expressed by the embryonic
 CC stem cell; (c) forming a culture comprising embryonic stem cells and the
 CC ligand; and (d) growing the cell culture. Also included are: (1)
 CC Modulating the differentiation of embryonic stem cells, comprising: (a)
 CC providing a cell transfected with a nucleic acid molecule selected from:
 CC (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic
 CC acid molecule that hybridises to the nucleic acid in (i), and which
 CC encodes a ligand capable of modulating embryonic stem cell
 CC differentiation, or capable of binding a Wnt receptor; or (iii) nucleic
 CC acid molecules which are degenerate as a result of the genetic code to
 CC the sequences of (i) or (ii); (b) forming a culture comprising the cell
 CC identified in (a) with an embryonic stem cell; and (c) growing the
 CC culture for the maintenance and/or differentiation of the embryonic stem
 CC cell; (2) Inhibiting the differentiation of embryonic stem cells,
 CC comprising: (a) providing at least one polypeptide or its active
 CC fragment, that are inhibitors of the Wnt signalling pathway; (b) forming
 CC a culture comprising the cell identified in (a) with an embryonic stem
 CC cell; and (c) growing the culture for the maintenance of embryonic stem
 CC cells in an undifferentiated state; or (3) Inhibiting the differentiation
 CC of embryonic stem cells, comprising: (a) providing a cell transfected
 CC with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt
 CC inhibitory polypeptide; (ii) a molecule which hybridises to the molecule
 CC of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;
 CC and (iii) nucleic acid molecules which are degenerate as a result of the
 CC genetic code to the sequences of (i) or (ii); (b) forming a culture
 CC comprising the cell identified in (a) with an embryonic stem cell; and
 CC (c) growing the culture for the maintenance of embryonic stem cells in an
 CC undifferentiated state; and (4) A cell, therapeutic cell or cell culture
 CC obtainable by any of the methods cited above. The therapeutic cell of the
 CC present invention is useful in the treatment of an animal, preferably a
 CC human, comprising administering a cell composition comprising embryonic
 CC stem cells which have been induced to differentiate into at least one
 CC cell-type. The cell is also useful for the manufacture of a composition
 CC for use in treatment of diseases such as Parkinson's disease,
 CC Huntington's disease, motor neuron disease, heart disease, diabetes,
 CC liver disease (e.g. cirrhosis), renal disease and AIDS (acquired
 CC immunodeficiency syndrome). The present sequence is represents a Wnt or
 CC Notch pathway protein (i.e. a ligand for the method of the invention)

XX	SQ	Sequence	722 AA;
XX	Query Match	72.9%; Score 2466; DB 6; Length 722;	
XX	Best Local Similarity	76.6%; Pred. No. 3.7e-112;	
XX	Matches	553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;	
QY	1	MGR-----LLASALLC---VSGVFELKLOEPVKKGLL--NRNCCRGG-----GCCTFFR	45
DB	1	MGRSALALAVVVSALLCQVWSSGVFELKLOEPVKKGLLGNRNCCRGSGGPPCAKWTFFR	60
QY	46	VCLKHYSQASVSPEPCTYGSA--TPVLG--SFS--PDGAG--DPAFSPNPIRPFPTWPGTFS	100
DB	61	VCLKHYSQASVSPEPCTYGSATVPLGVDSFSLPDGAGIDPAFSPNPIRPFPTWPGTFS	120
QY	101	LIIEALHTDSPDDL--TENPERLISRL--TORHL--VGEWESQDLHSSGRTDL--YSYRPFVDE	156
DB	121	LIIEALHTDSPDLATENPERLISRLTTORHLTVGEWESQDLHSSGRTDLRYSYRPFVDE	180
QY	157	HYGEGCSVFCRPRDD--FGHFTCG--RGEK--C--PGMKGOYCT--PICLPGC--DOHG--CDKPG	209
DB	181	HYGEGCSVFCRPRDDAFGHFTCGRGEKMDPGWKQYCTDPICLPGCDDQHGICYDKPG	240
QY	210	ECKCRVGMQGRYCDCEIRYPGCVHGTCCQPMQCNQCEGGLFCNQDLNYCTHHKPC--NG	268
DB	241	ECKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGGLFCNQDLNYCTHHKPCRN	300
QY	269	ATCTNTGGSYTCSCRPGYTG--CE---EBC---PCKNG--SCTDLES---SCTCPGPFYK	317
DB	301	ATCTNTGGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFCTCPGPFYK	360
QY	318	-CELSAMTCADGCPFNCGRC--DNPDDGY--C--CPLG--SGFNCEKKD--C--SSPC--NGA--CV	367
DB	361	VCELSAMTCADGCPFNCGRCSDNPDGTYCHCPLGFGFNCEKKMDLGGSSPSCNGAKCV	420
QY	368	DIGNSY-C--COAGF--GR--C--DNVDDCA--SPC--NGGTC--DVND--SCTCPPGY--GKNC	415
DB	421	DIGNSYLCRCQAGFSRYCEDNVDDCASSPCANGTCDSDVNDVNDVNDVNDVNDVNDVND	480
QY	416	VSRCH--PCHNGATCHRR-----YCSCA--GYGG--NQCFLLPE--PPGP--VD-----	458
DB	481	VSRCHPCHNGATCHQGRQYMCQAQYQYMCQAQYQYMCQAQYQYMCQAQYQYMCQAQY	540
QY	459	--FPW--AVCAGLV---LILLGCAA--VVCRLK--QK---PE--C--ETETMNNLANCQREK	503
DB	541	GPFPWAVCAGVLLVLLGCAAVVVCRLKQKHQPPPEPCGGTETMNNLANCQREK	600
QY	504	D---SSIGATQIKNTNKK--DFHDK-----KVRYP--VDYNLV--LK-----VHKK	540
DB	601	DVSVSIIIGATQIKNTNKKADFHGDHGAKKSPKVRYPVDYNLVRLDKGDEATVRDTHSK	660
QY	541	-----CSEKAL-----RKRP--SVYSTSKDTKYQSVYV---SEKDEC--IAT	576
DB	661	RDTKQSSQSSAGEEKIAPTARGEIPDRKRPSVYSTSKDTKYQSVYVLSAEKDECVIAT	720
QY	577	EV 578	
DB	721	EV 722	
XX	RESULT 7		
XX	AAE34029		
XX	ID	AAE34029 standard; protein; 722 AA.	
XX	AC	AAE34029;	
XX	DT	02-MAY-2003 (first entry)	
XX	DE	Murine notch ligand delta-like 1 protein.	
XX	KW	Murine; drug screening; toxicology assay; signalling pathway;	
XX	KW	notch ligand delta-like 1.	

OS Mus sp.
XX WO200290992-A2.
XX 14-NOV-2002.
XX 29-APR-2002; 2002WO-GB001946.
XX 04-MAY-2001; 2001GB-00011004.
XX (AXOR-) AXORDIA LTD.
XX Andrews P, Draper J, Walsh J;
XX WPI; 2003-120579/11.
XX N-PSDB; AAD52523.
XX Identifying biologically active agents comprises cloning transfected
PT cells into a cell array, exposing the array to an agent to be tested, and
PT detecting signals generated by a reporter molecule as a result of
PT exposure to the agent.
XX Claim 16; Fig 2; 90pp; English.
XX The present invention relates to a novel screening method which enables
CC the identification of biologically active agents which mediate their
CC effect through the activation of genes. The method involves providing a
CC population of cells stably transfected with a nucleic acid encoding a
CC reporter molecule, cloning the transfected cells into a cell array,
CC exposing the array to at least one agent to be tested and detecting a
CC signal generated by the reporter molecule as a result of exposure to the
CC agent. The method is useful in identifying biologically active agents and
CC the genes through which the agents act, in screening potential drugs for
CC their ability to activate certain drug targets in a high-throughput
CC assay, in identifying relationships between signalling pathways and
CC specific signals that could be useful in eventually directing the
CC differentiation of embryonic stem cells and in toxicology assays by
CC testing for unwanted activation or inhibition of specific signalling
CC pathways. The present sequence is murine notch ligand delta-like 1
CC protein used to illustrate the method of the invention
XX
SQ Sequence 722 AA;
Query Match 72.9%; Score 2466; DB 6; Length 722;
Best Local Similarity 76.6%; Pred. No. 3.7e-112;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;
QY 1 MGR-----LLASALLC-----VSGVFELKQBFVNKGLL-NRNCRRG-----GCCTFFR 45
DB 1 MGRSALALAVSALLCQVMSVGFELKQBFVNKGLLGNRNCRRGSGPPCACRTFFR 60
QY 46 VCLKHYQASVSEPPCTYGA-TPVLG--SFS-PDGAG-DPAFNPFRFPGFTWPGTES 100
DB 61 VCLKHYQASVSEPPCTYGA-TPVLG--SFS-PDGAG-DPAFNPFRFPGFTWPGTES 120
QY 101 LIIEALHTDPPDDL-TENPERLISRL-TQRHL-VGEWSDQLHSSGRDIL-YSYRFVCD 156
DB 121 LIIEALHTDPPDLATENPERLISRL-TQRHL-VGEWSDQLHSSGRDILYSYRFVCD 180
QY 157 HYEGGCVSRCPRDD-FGHTCG-RGEK-C-PWKGOYCT-PICLPGC-DQHG-CDKPG 209
DB 181 HYEGGCVSRCPRDDAFGHFTCTDGRGKMDPGWKQYCTDPTICLPGCDQHGCDKPG 240
QY 210 ECKCRVGMQRYCDECIYPCGVHGTQOPQCNQCGWGLFCNODLNYCTHHKPC-NG 268
DB 241 ECKCRVGMQRYCDECIYPCGLHGTCCQPMQCNQCGWGLFCNODLNYCTHHKPCNG 300
QY 269 ATCTNTGGSYTCSCRPYTG--CE---EEC---PCNKG-SCTDLES--SCTCPPGFYGK 317
DB 301 ATCTNTGGSYTCSCRPYTGANCELEVDCAFPCKNGASCTDLESFSCCTCPPGFYGK 360
QY 318 -CELSAMTCADGPFNGGRC-DNPDGY-C-CPIUG-SGFNCEKDD--C-SSPC-NGA-CV 367
|||||

Db 361 VCELSAMTCADGPFNGGRCSDNPDDGYTCHCPLGFGFNCCKKMDLCSGSPCSNGAKCV 420
QY 368 DLGNSY-C-COAGF-GR-C-DNVDCA-SPC-NGGTC--DNVD-SCTCPPGY-GRNCS-P 415
DB 421.DLGNSYLCRCOAGFSGRYCEDNVDCCASSCANGTCRDSVNDSCCTCPPGYTGNCSAP 480
QY 416 VSRCEH-PCNHGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----BEQ- 458
DB 481 VSRCEHAPCHNGATCHQGRQYMCCECAQGYGPNQCQLLPPPPGPMVVDLSERHMSQG 540
QY 459 --PPM-AVCAGLV---LLLLGCA--VVCVRLK-QK-----PE-C--ETETNNLANCQREK 503
DB 541 GPPFWAVACAGVLLVLLLLGCAAVVVCVRLKQHPPEPCGGETETMNNLANCQREK 600
QY 504 D---SSIGATQIKNTKK-DPHDK-----KVRYF-VDYNLV--LK-----VHKK 540
DB 601 DVSVSIIIGATQIKNTKKADPHGDHGAKSFSKRYPTVDYNLVRLDKGDEATVDRDTHSK 660
QY 541 -----CSBEKAL-----RKRP-SVYSTSKTKYOSVYV--SEKDEC-IAT 576
DB 661 RDTKCQSSAGBEKIAPTLRGGEIPDKRPESVYSTSKTKYOSVYVLSAEKDECVIAT 720
QY 577 EV 578
DB 721 EV 722
RESULT 8
AAW18353
ID AAW18353 standard; protein; 723 AA.
XX AAW18353;
XX AC
XX DT 11-FEB-1998 (first entry)
XX DE Proliferation and differentiation suppression polypeptide.
XX KW Proliferation; differentiation; suppression; human; delta-1; serrate-1;
KW blood cell; neuron; leukaemia; malignant tumour; immunosuppression.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= Signal
FT /label= Differentiation_suppression_protein
XX WO9719172-A1.
XX 29-MAY-1997.
XX 15-NOV-1996; 96WO-JP003356.
XX 17-NOV-1995; 95JP-00299611.
XX 30-NOV-1995; 95JP-00311811.
XX (ASAH) ASAH KASEI KOGYO KK.
XX Sakano S, Itoh A;
XX WPI; 1997-298110/27.
XX N-PSDB; AAT70174.
XX Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress
PT proliferation and differentiation of undifferentiated human blood cells.
XX Claim 15; Page 77-82; 114pp; Japanese.
XX The present sequence represents a polypeptide which suppresses
CC proliferation and differentiation of undifferentiated cells such as
CC neurons and blood cells. The polypeptide may be used for the prevention
CC and control of disorders involving undifferentiated cells, such as

Db 553 ILVLLGLGCAAVVYVRLRLQKHPPADPCRGETETMNNLANCOREKDISVSIIGATQI 612
Qy 513 KNTNKK-DHF-----DK---KVRYP-VYNNLV-----LKVHKKC-----S 542
Db 613 KNTNKKADFGHDSADKNGFKARYPAVDYNNLVQDLKGGDDTAVRDAHSKRTKCPQSSG 672
Qy 543 EEKAL-----RKRP-SVYSTSKDTKYQSVV---SEKDEC-IATEV 578
Db 673 EEKGTPTTLRGEASERKRPDSCGTSKDTKYQSVVYVISEEKDECVIATEV 723

RESULT 10
AAW94498
ID AAW94498 standard; protein; 723 AA.

XX AC AAW94498;

XX 22-APR-1999 (first entry)

XX Human delta-1 protein.

XX Human; delta-1; delta-2; differentiation inhibitor; proliferation;
XX leukaemia; malignant tumour.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..21

XX Protein /label= signal

XX FT 22..723

XX FT /label= Delta-1

XX WO9851799-A1.

XX 19-NOV-1998.

XX 13-MAY-1998; 98WO-JP002104.

XX 14-MAY-1997; 97JP-00124064.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Sakano S;

XX WPI; 1999-070120/06.

XX N-PSDB; AAX16300.

XX Peptide inhibiting the differentiation of undifferentiated blood - used
XX for treatment of cancer and other disorders and the culture of human
XX cells in vitro.

XX Example 1; Page 64-69; 86pp; Japanese.

XX The present invention describes full length and shortened human delta-2
XX proteins. Human delta-2 is a differentiation inhibitor which inhibits the
XX differentiation of undifferentiated cells (other than brain or muscle
XX cells), such as blood cells, and enhances the proliferation of
XX undifferentiated blood cells. Products of human delta-2 may be used for
XX the treatment of diseases such as leukaemia and malignant tumours. They
XX may also be used in the culture of human cells in vitro, e.g. for
XX production of supplies of undifferentiated blood cells. The present
XX sequence represents human delta-1, from an example of the present
XX invention

XX Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 2; Length 723;
Best Local Similarity 75.1%; Pred. No. 5e-109;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

Qy 7 SALLIC---VSGVFELKQEFVNNKKGLL-NRNCRRG-----GCCTFRVCLKHYQASVS 56
||||| ||||||||||||||||||| |||||||

Db 13 SALLICQVWSSGVFELKQEFVNNKKGLLNRNCRGAGPPPCACKTFRFVCLKHYQASVS 72
Qy 57 PEPCTYGS-A-TPVLG--SFS-PDGAG-DPAFNPPIRPFPGFTWPGTFSLLIEALHTDSP 111
Db 73 PEPCTYGS-A-TPVLG--SFS-PDGAG-DPAFNPPIRPFPGFTWPGTFSLLIEALHTDSP 132
Qy 112 DDL-TEMPERLISRL-TORHL-VGEWSQDLHSSGRTDL-YSRPVCDEHYHGECSVFC 167
Db 133 DDLATENPERLISRLATORHLTVGEWSQDLHSSGRTDLKYSYRFPVCDEHYHGECSVFC 192
Qy 168 RPRDD-FGHFTCG-RGEK-C-PGWKQYCT-PICLPQCD-QHG-CDRPGCEKCRVGMQGR 220
Db 193 RPRDDAFGHFTCGRGEKVCNPNWKGYPCTEPICLPGCDEQHGCDRPGCEKCRVGMQGR 252
Qy 221 YCDECIRYPGVCHGTCCQPMQCNQCEGMGGLFCNQDLNYCTHHKPC-NGATCTTNGQGSY 279
Db 253 YCDECIRYPGLHGTCCQPMQCNQCEGMGGLFCNQDLNYCTHHKPCNGATCTTNGQGSY 312
Qy 280 TCSCRPGYTG--CE---BEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327
Db 313 TCSCRPGYTGATCBLGIDECOPSPCKNGGSCDTDLENSYSCTCPGFGYKICELSAMTCAD 372
Qy 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSDC-NGA-CVDLGSY-C-CQ 376
Db 373 GPCFNGGRCSDSPDGGYSCRCPVGSGFNCEKKIDYCSSSPCSNGAKCVDLDGAYLCRCQ 432
Qy 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425
Db 433 AGFSGRHCDNDVDDCASSPCANGTCDRGVNDPFCCTCPGTYGRNCSAPVSRCEHAPCHN 492
Qy 426 GATCHRR-----YCECA-GYGG-NCQFLLE-PPGP--VD-----EQ---FPW-AVCAGL 467
Db 493 GATCHERGHRYVCECARGYGGPNCQFLLEPPGPVVDLTKLEGGGGPPFWAVCAGV 552
Qy 468 VL---LLLGCAA-VVCVRL---KQPEC-----ETETMNNLANCOREKDISVSIIGATQI 512
Db 553 ILVLLGLGCAAVVYVRLRLQKHPPADPCRGETETMNNLANCOREKDISVSIIGATQI 612
Qy 513 KNTNKK-DHF-----DK---KVRYP-VYNNLV-----LKVHKKC-----S 542
Db 613 KNTNKKADFGHDSADKNGFKARYPAVDYNNLVQDLKGGDDTAVRDAHSKRTKCPQSSG 672
Qy 543 EEKAL-----RKRP-SVYSTSKDTKYQSVV---SEKDEC-IATEV 578
Db 673 EEKGTPTTLRGEASERKRPDSCGTSKDTKYQSVVYVISEEKDECVIATEV 723

RESULT 11

AAW93227

ID AAW93227 standard; protein; 723 AA.

XX AC AAW93227;

XX 16-AUG-2000 (first entry)

XX PRO172 Polypeptide.

XX Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;
XX uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;
XX leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..21

XX Modified-site 2..8

XX /note= "N-myristoylation site"

XX Modified-site 37..43

XX /note= "N-myristoylation site"

XX Modified-site 40..46

XX /note= "N-myristoylation site"

XX Modified-site 93..97

FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	98. .104
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	99. .105
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	131. .135
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	154. .158
FT	Modified-site	/note= "Casein kinase II phosphorylation"
FT	Modified-site	176. .185
FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"
FT	Modified-site	203. .207
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Domain	243. .255
FT	Modified-site	/label= EGF-like_domain
FT	Modified-site	252. .261
FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"
FT	Modified-site	262. .268
FT	Domain	/note= "N-myristoylation site"
FT	Modified-site	274. .286
FT	Modified-site	/note= "EGF-like domain"
FT	Modified-site	281. .287
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	282. .288
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	301. .307
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	310. .316
FT	Modified-site	/note= "N-myristoylation site"
FT	Domain	314. .326
FT	Modified-site	/label= EGF-like_domain
FT	Modified-site	328. .334
FT	Modified-site	/note= "N-myristoylation domain"
FT	Modified-site	340. .346
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	342. .346
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	343. .355
FT	Modified-site	/note= "Asn and Asp hydroxylation site"
FT	Modified-site	344. .348
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Domain	352. .364
FT	Modified-site	/label= EGF-like_domain
FT	Modified-site	369. .373
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	378. .384
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	387. .393
FT	Modified-site	/note= "N-myristoylation site"
FT	Domain	391. .403
FT	Modified-site	/label= EGF-like_domain
FT	Modified-site	420. .432
FT	Domain	/note= "Asn and Asp hydroxylation site"
FT	Modified-site	429. .441
FT	Modified-site	/label= EGF-like_domain
FT	Modified-site	457. .461
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	458. .480
FT	Domain	/label= Asn and Asp hydroxylation site
FT	Modified-site	467. .479
FT	Modified-site	/label= EGF-like_domain
FT	Modified-site	477. .481
FT	Modified-site	/note= "N-glycosylation site"
FT	Modified-site	483. .487
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	495. .499
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Domain	505. .517
FT	Modified-site	/label= EGF-like_domain
FT	Modified-site	512. .518
FT	Modified-site	/note= "N-myristoylation site"
FT	Domain	548. .568
FT	Modified-site	/label= Transmembrane domain

FT	Binding-site	552..563	/label= Prokaryotic membrane lipoprotein lipid attachment site
FT	Modified-site	659..663	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	660..664	/note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT	Modified-site	670..674	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	671..675	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	676..682	/note= "N-myristoylation site"
FT	Modified-site	683..689	/note= "N-myristoylation site"
FT	Modified-site	695..701	/note= "N-myristoylation site"
FT	Modified-site	698..702	/note= "Casein kinase II phosphorylation site"
XX		WO200021996-A2.	
XX		20-APR-2000.	
XX		05-OCT-1999;	99WO-US023089.
XX		13-OCT-1998;	98US-0104080P.
XX		(GETH) GENENTECH INC.	
XX		Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WJ; Yuan J;	
XX		WPI; 2000-317943/27.	
DR		N-PSDB; AAZ93703.	
XX		Composition for inhibiting neoplastic cell growth and treating cancers of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist.	
PT		Claim 12; Fig 8; 122pp; English.	
XX		Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia	
XX		Sequence 723 AA;	
SQ		Query March 71.0%; Score 2401.5; DB 3; Length 723;	
		Best Local Similarity 75.1%; Pred. No. 56-109;	
		Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67	
Qy		7 SALLAC---VSGVFELKLQEFVNKKGLL-NRNCRRG-----GCCTFFRVLCKHYQASVS 56	
Db		13 SALLCQWSSGVFELKLQEFVNKKGLLGNRNCRRGAGPPPCACRTFFRVLCKHYQASVS 72	
Qy		57 PEPPTCYGSA-TPVLG--SFS-PDGAG-DPAFNSPIRFPFGTWPGTFSLLIEALHTDSP 111	
Db		73 PEPPTCYGSAVTPVLGVDSFSLPDGGGADSAFNSPIRFPFGTWPGTFSLLIEALHTDSP 132	
Qy		112 DDL-TEMPERLISRL-TORHL-VGEHWSODLHSGRTDL-VSYRVCDEHYHGECSVFC 167	
Db		133 DDLATENPERLISRLATQRHLTVGEHWSQDLHSGRTDLKYSYRVCDEHYHGECSVFC 192	
Qy		168 RPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPQCD-QHG-CDKPGCKRCRVGWGR 220	
Db		193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEHGFCDKFGCKRCRVGWGR 252	
Qy		221 YCDECIRYPGVCHGTCCQPPWCNCOEGGGLFCNQDLNLYCTHHKPC-NGATCTNTGQGSY 279	

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Db 253 YDCBIRYPGCLHGTCCQPMOCNCEQWGGGLFCNQDLNYCTHHKPKNGATCTNTGQGSY 312
Qy 280 TCSRCPGYTG--CE---BEC---PCKN--GSCTDLDES--SCTCPGFGYK--CELSAMTCAD 327
Db 313 TCSRCPGYTGATCGLGIDECDFSPCKNGSGCTDLSENSYCTCPGFGYKICELSAMTCAD 372
Qy 328 GPCFNGGRGRC-DNPGGY-C-CPLG-SGFNCBKK---DCSSPC-NGA-CVDLGNYSY-C-CQ 376
Db 373 GPCFNGGRGRCSDPGGYSCRCFVGSGFNCBKKIDYCSSSPCSNGAKCVDLGLDAYLCRCQ 432
Qy 377 AGF--GR-C-DNVDCA-SPC-NGGTC--DNVD-SCTCPGPGY-GKNCS-PVSRCEH-PCNN 425
Db 433 AGFSGRHDDNVDCA-SPC-NGGTC--DNVD-SCTCPGPGY-GKNCS-PVSRCEH-PCNN 492
Qy 426 GATCHRR----YCECA-GYGG-NQQLLPE-PPGP--VD-----EQ-----PPM-AVCAGL 467
Db 493 GATCHERGRVYCECARGYGGPNCQFLPELPPGPAVVDLTKELGGQGGPPFWAVCAGV 552
Qy 468 VL-----LLIGCAA-VVTVRL-----KQPEC-----ETETNNLANCOREKD---SSIGATQI 512
Db 553 ILVLLMLLGCAAVVTVRLQLQHRPPADPCRGETETNNLANCOREKDISVSIIGATQI 612
Qy 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542
Db 613 KNTNKADFGHDSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQFQSSG 672
Qy 543 EEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IADEV 578
Db 673 EEKGTPTTLRGGEASERKRPDSGSGSTSKDTKYQSVYVISEKDECVIATEV 723

RESULT 12
AAB33422
ID AAB33422 standard; protein; 723 AA.
AC AAB33422;
XX
XX 29-JAN-2001 (first entry)
XX Human PRO172 protein UNQ146 SEQ ID NO:41.
XX Human; immune related disease; diagnosis; antinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antiparasitic; antiallergic;
KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; hepatobiliary disease; enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX Homo sapiens.
XX
XX W0200053758-A2.
XX
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005841.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
XX 12-MAR-1999; 99US-0123957P.
XX 23-MAR-1999; 99US-0125775P.
XX 12-APR-1999; 99US-0128849P.
XX 20-APR-1999; 99WO-US008615.
XX 28-APR-1999; 99US-0131445P.
XX 04-MAY-1999; 99US-0132371P.
XX 14-MAY-1999; 99US-0134287P.
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PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
XX Kabakoff RC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V;
XX Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX WPI; 2000-572271/53.
XX N-PSDB; AAC58587.
XX
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
XX Claim 33; Fig 18; 309pp; English.
XX
XX The present invention describes sixty four human PRO proteins which can
XX be used in the treatment of immune related diseases. The human PRO
XX proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX treating and diagnosing immune related disorders. The disorders are
XX selected from systemic lupus erythematosus, rheumatoid arthritis,
XX osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX immune-mediated renal disease, demyelinating diseases of the central and
XX peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
XX disease, gluten-sensitive enteropathy and Whipple's disease. Autoimmune
XX or immune-mediated skin diseases, allergic diseases, immunological
XX diseases of the lung, and transplantation associated diseases including
XX graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
XX represent PCR primers and hybridisation probes used in the isolation of
XX human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
XX represent human PRO polynucleotide and protein sequences given in the
XX exemplification of the present invention
XX
XX Sequence 723 AA;
```

Query Match 71.0%; Score 2401.5; DB 3; Length 723;

Best Local Similarity 75.1%; Pred. No. 5e-109;

Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

Qy 7 SALLC---VSGVFELKLQEFVNKKGLL-NRNCRCG-----GCCTFFRVCLKHYQASVS 56

```
Db 13 SALLCQWSSGVFELKQLQEFVNKKGLLGNRNCRCGGAGPPPCACRTFFRVCLKHQOASVS 72
QY 57 PPPCTYGSAA-TPVLG--SFS-PDGAG-DPAFSPNIRPFPGFTWPGTFFSLIIALHTDSP 111
Db 73 PPPCTYGSAAVTPVLGVDSFSLPDGGGADSAFSPNIRPFPGFTWPGTFFSLIIALHTDSP 132
QY 112 DDL-TENPERLISRL--TORHL--VGEWSODLHSSGRTDL--YSYRFVCDDEHYHGGGCVFC 167
Db 133 DDLATENPERLISRLATQRLHTLVGEWSODLHSSGRTDLKYSYRFVCDDEHYHGGGCVFC 192
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PTCLPGCD-QHG-CDKPGCKRCRVGQGR 220
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPCTEPICLPGCDEQHGFCDDKPGCKRCRVGQGR 252
QY 221 YDECIIRPGCVHGTCCQWPQNCQBGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279
Db 253 YDECIIRPGCLHGTCCQWPQNCQBGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY 312
QY 280 TCSRCRGYTG--CE---EBC---PCKN-GSCTDLES--SCTCPGPGYVK-CELSAMTCAD 327
Db 313 TCSRCRGYTGATCELGIDBCDPSCKNGSGCTDLENSYSCTCPGPGYKICELSAMTCAD 372
QY 328 GPCFNGGRC-DNPDGYY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYS-C-CQ 376
Db 373 GPCFNGGRCSDPDGYSRCPCVGYSGFNCCKIDYCSSSPCSNGAKCYDLGDAYLCRCQ 432
QY 377 AGF-GR-C-DNVDCA-SPC-NGGTC--DVND-SCTCPGYY-GKNC-S-PVSRCEH-PCNH 425
Db 433 AGPSGRHCDNDVDCASSPCANGGTCRDGVNDFSCTCPGYYTGRNCSAPVSRCEHAPCHN 492
QY 426 GATCHRR---VCECA-GYGG-NCQELLPE-PRGP--VD-----EQ---FWM-AVCAGL 467
Db 493 GATCHERHRYVCECARGYGGNQCQLLPELPGPAVDLTKLEGQGGFFPWWAVACAGV 552
QY 468 VL---LLLGCAA-VVVCRL---KQKPEC-----ETETMNLANCOREKD---SSIGATQI 512
Db 553 ILVLMLLGCAVVCVRLQLQHRPPADPCRGETETMNLANCOREKDISVSIIGATQI 612
QY 513 KNTNKK-DHF-----DK---KVRYP--VDYNLV-----LKVHKKC-----S 542
Db 613 KNTNKADEFHDSADKNGFKARYPAVDYNLVQDLKGGDDTAVRDAHSKRDTKCQPOGSSG 672
QY 543 EEKAL-----RKRP-SVYSTSKDTKYOSVVV--SEKDEC-IATEV 578
Db 673 EKGTTTLRGEASERKRPDSCSTSKDTKYOSVYVISEEKDECVIATEV 723
```

RESULT 13

AAB24388
ID AAB24388 standard; protein; 723 AA.

XX AAB24388;

XX 07-NOV-2000 (first entry)

DE Human PRO172 protein sequence SEQ ID NO:4.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiatic; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.

OS Homo sapiens.

XX W0200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1998; 98WO-US025108.

PR 16-DEC-1998; 98US-0112850P.

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PR 12-JAN-1999; 99US-0115554P.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99US-0134287P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 29-OCT-1999; 99WO-US023089.  
PR 25-OCT-1999; 99US-0162508P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;  
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;  
PI Smith V, Watanabe CK, Williams PW, Wood WI;  
XX  
DR WPI; 2000-412154/35.  
N-PSDB; AAA77512.
```

Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating a cardiovascular, endothelial or angiogenic disorders in mammals.

Claim 72; Fig 2; 315pp; English.

The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating a disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention

Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 3; Length 723;
Best Local Similarity 75.1%; Pred No 5e-109;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFEKLQEFVNKKGLL-NRNCRCG-----GCCTFFRVCLKHQOASVS 56

Db 13 SALLCQWSSGVFELKQLQEFVNKKGLLGNRNCRCGGAGPPPCACRTFFRVCLKHQOASVS 72

QY 57 PPPCTYGSAA-TPVLG--SFS-PDGAG-DPAFSPNIRPFPGFTWPGTFFSLIIALHTDSP 111

Db 73 PPPCTYGSAAVTPVLGVDSFSLPDGGGADSAFSPNIRPFPGFTWPGTFFSLIIALHTDSP 132

QY 112 DDL-TENPERLISRL--TORHL--VGEWSODLHSSGRTDL--YSYRFVCDDEHYHGGGCVFC 167

Db 133 DDLATENPERLISRLATQRLHTLVGEWSODLHSSGRTDLKYSYRFVCDDEHYHGGGCVFC 192

QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PTCLPGCD-QHG-CDKPGCKRCRVGQGR 220

Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPCTEPICLPGCDEQHGFCDDKPGCKRCRVGQGR 252

QY 221 YDECIIRPGCVHGTCCQWPQNCQBGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279

Db 253 YDECIIRPGCLHGTCCQWPQNCQBGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY 312

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QY 280 TCSRPVGTG--CE---BEC---PCKN-GSCTDLSES--SCTCPGFGYK-CELSAMTCAD 327
DQ 313 TCSRPVGTGATCELGIDECPSCKNGSGCTDLSESYCTCPGFGYKICELSAMTCAD 372
QY 328 GPCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376
DQ 373 GPCFNGRCSDSPDGGYSCRCFVSGFNCCKKIDYCSSPCNGAKCVDLGDAYLCRCQ 432
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPGPGY-GKNCS-PVSRCEH-PCHN 425
DQ 433 AGFSGRHCDNDVDDCASSPCANGTCRGVNDPFCCTCPGPGYGRNCSAPVSRCEHAPCHN 492
QY 426 GATCHRR-----YCECA-GYGG-NCQFLPPE-PPGP--VD-----BEO---FPW-AVCAGL 467
DQ 493 GATCHERGHRYVCEARGYGGFNCQFLPPELPPGPVAVDLTEKLEGGGPPFWAVCAGV 552
QY 468 VL---LLLGCAA-VVYVRL---KQPEC-----ETETMNNLANCOREKD---SSIGATQI 512
DQ 553 ILVLLMLLGGCAAVVYVRLQKRRPPADPCRGGETETMNNLANCOREKDISVSIIGATQI 612
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542
DQ 613 KNTNKKADFHGDHSDKNGFKARYPAVDYNLVQDLKGGDTAVRDAHKKRDTKQPGSSG 672
QY 543 EEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEB-IATEV 578
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RESULT 14

AY79032 standard; protein; 723 AA.

AY79032;

06-JUN-2000 (first entry)

Human delta protein amino acid sequence.

Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;
lung; melanoma; seminoma; central nervous system disorder; psoriasis;
tissue regeneration; liver cirrhosis; keloid formation; baldness;
inner ear disorder; human.

Homo sapiens.

W0200002897-A2.

20-JAN-2000.

13-JUL-1999; 99WO-US015817.

13-JUL-1998; 98US-0092513P.

19-OCT-1998; 98US-0104834P.

(UYUA) UNIV YALE.

Artavanis-Teakonas S, Rand MD, Qi H;

WPI; 2000-282852/24.

N-PSDB; AAZ98679.

New cleavage peptide, nucleic acids and antibodies useful for diagnosis,
prevention and treatment of cancer, disorders of central nervous system,
cirrhosis and psoriasis.

Claim 1; Fig 4; 177pp; English.

This sequence represents the human delta protein amino acid sequence.
Delta is a topotypic protein that contains a sequence which is cleaved
by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz
results in two fragments, a soluble amino terminal fragment consisting
essentially of the extracellular domain, and a membrane bound fragment

consisting of the transmembrane domain and the intracellular domain. The
soluble fragment is able to bind to Notch. Delta plays a key role in
differentiation, and therefore detection and measurement of delta
activation is important in the study of differentiation. The invention
relates to the delta cleavage peptides (the active fragment), and to
methods for detecting and measuring delta activation. Delta cleavage
peptides, and chimeric proteins are useful for modulating the activity of
Notch, delta or kuz or at least one of the signalling pathways in a cell
or organism, expressing Notch. By contacting a cell with kuz protein or
nucleic acid or its antibody, the activity or levels of delta protein is
modulated and vice versa. A delta cleavage peptide or its derivative
capable of binding kuz protein is useful for treating or preventing a
disease or disorder associated with increased delta activity or
expression such as cervical, breast, colon or lung cancer, melanoma or
seminoma in humans. A recombinant cell comprising a delta peptide is
useful for treating or preventing central nervous system disorders. A
delta cleavage peptide is useful for the diagnosis of diseases or
disorders associated with increased levels of Notch-delta protein binding
activity comprising measuring the ability of delta cleavage peptides in a
sample to bind kuz protein. A complex of delta protein and kuz is useful
for diagnosing or screening for the presence of, or predisposition to
developing a disease or disorder associated with aberrant levels of the
complex, comprising measuring the level or functional activity of the
complex or RNA encoding delta or kuz in a sample. The delta cleavage
peptide is also useful for promoting tissue regeneration and repair, for
treating liver cirrhosis, keloid formation, psoriasis, baldness and
degenerative or traumatic disorders of the sensory epithelium of the
inner ear

Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 3; Length 723;

Best Local Similarity 75.1%; Pred. No. 5e-109;

Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

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DQ 133 DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDHYHYGGCSVFC 192
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DQ 373 GPCFNGRCSDSPDGGYSCRCFVSGFNCCKKIDYCSSPCNGAKCVDLGDAYLCRCQ 432
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AAB00172				
ID	AAB00172	standard; protein; 723 AA.		
XX	AAB00172;			
DT	08-FEB-2001	(first entry)		
XX	PRO172	polypeptide.		
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KW	treatment; therapy; agonist; antibody; breast cancer;	ovarian cancer;		
KW	renal cancer; colorectal cancer; uterine cancer;	prostate cancer;		
KW	lung cancer; bladder cancer; melanoma; leukaemia;	inflammatory disorder;		
KW	angiogenic disorder; immunologic disorder; human.			
OS	Homo sapiens.			
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XX	WO2000055319-A1.			
PN	21-SEP-2000.			
PD	02-DEC-1999;	93WO-US028564.		
XX	12-MAR-1999;	93US-0123957P.		
PR	28-APR-1999;	93US-0131445P.		
PR	20-JUL-1999;	93US-0144758P.		
PR	26-JUL-1999;	93US-0145698P.		
PR	08-SEP-1999;	93WO-US020594.		
PR	15-SEP-1999;	93WO-US021090.		
PR	05-OCT-1999;	93WO-US023089.		
PR	30-NOV-1999;	93WO-US028313.		

XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
XX PI Yuan J;
XX DR WPI; 2000-638201/61.
XX DR N-ESDB; AAA54105.
XX PT PRO211, PRO228, PRO338, PRO172 and PRO182 polypeptides useful for
XX PT treating tumors including cancers of the breast and lung leukemia and
XX PT for identifying compounds capable of inhibiting growth of neoplastic
XX PT cells.
XX PS
XX PS Claim 31; Fig 8; 133pp; English.
XX CC Isolated PRO211, PRO228, PRO338, PRO172 or PRO182 polypeptides or their
XX CC agonists (preferably anti-PRO agonist antibody or a small molecule
XX CC mimicking the biological activity of PRO polypeptide) are useful in vitro
XX CC or in vivo for inhibiting the growth of a tumour cell. Compositions
XX CC comprising the PRO polypeptides are useful for inhibiting neoplastic cell
XX CC growth and for treating cancer including breast, ovarian, renal,
XX CC colorectal, uterine, prostate, lung, bladder, central nervous system
XX CC cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also
XX CC useful for treating other disorders such as neuronal, glial, astrocytal,
XX CC hypothalamic and other glandular, macrophagal, epithelial, stromal,
XX CC blastocoealic disorders and inflammatory, angiogenic and immunologic
XX CC disorders as well as being useful for identifying agonists to PRO
XX CC polypeptides by contacting the polypeptide with a candidate molecule and
XX CC monitoring biological activity mediated by the polypeptide
XX SQ Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 3; Length 723;
Best Local Similarity 75.1%; Pred. No. 5e-109;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;
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Qy 57 PEPPCTYGS-A-TPVLG--SFS-PDGAG-DPAFNPPIRPFPGFTWPGTFSLIIEALHTDSP 111
Db 73 PEPPCTYGS-AVTPVLGVSFSLPDGGGADSAFNPPIRPFPGFTWPGTFSLIIEALHTDSP 132
Qy 112 DDL-TEMPERLISRL-TORHL-VGEWSODLHSSGRDYL-YSRFVCDHYHGGCSVFC 167
Db 133 DDLATENPERLISRLATQRLHVTGEEWSQDLHSSGRDYLKYSRPFVCDHYHGGCSVFC 192
Qy 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGCKCRVGMQGR 220
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKPYCTEPICLPGCDEQHGFCDKPGCKCRVGMQGR 252
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Job time : 64.7823 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:18:13 ; Search time 16.1897 Seconds
(without alignments)
2367.669 Million cell updates/sec

Title: US-09-783-931-13

Perfect score: 3383

Sequence: 1 MGRLLASALLCVSGVFELK.....DTKYQSVVSEKDECIATEV 578

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2462	72.8	722	3	US-08-981-392-12
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8	2454	72.5	720	3	US-08-872-855-4
9	2447.5	72.3	713	3	US-08-872-855-5
10	2401.5	71.0	723	3	US-09-068-740A-9
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ALIGNMENTS

RESULT 1
US-08-981-392-13
; Sequence 13, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antier, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-981-392-13

Query Match 100.0%; Score 3383; DB 3; Length 578;
Best Local Similarity 100.0%; Pred. No. 3.3e-245;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRLLASALLCVSGVFELKQLQEFVNKGLLRNCRGGGCTFFRVCLKHQYQASVSPPEP 60
Db |||||
QY 1 MGRLLASALLCVSGVFELKQLQEFVNKGLLRNCRGGGCTFFRVCLKHQYQASVSPPEP 60
Db |||||
QY 61 CTYGSATPVLSGSPDGAGDPAFSNPIRPFPGTWPFTSLIEALHTDSPDALTENPER 120
Db |||||
QY 121 LISRLTORHLVGEWSQDLHSSGRTDLYSYRFVCDDEHYHGECSVFCRPRDDFGHFTCCR 180
Db |||||
QY 181 GSKCPGWKQYCTPICLPGCDQHGCDKPECKCRVGMQGRYDCECIRYPCGVHGTCCQPM 240
Db |||||
QY 241 QCNQCEGWSGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSRPGYTGCBEPCCKNGS 300
Db |||||
QY 301 CTDLESSCTCPGFGYKCELSAMTADGFCFNGRCNDPDDGYYCCPLGSGFNCCKDCSS 360
Db |||||
QY 361 PCNGACVDLGNSSYCCQAGFGRCNDVDDCASPCNGGTCDVNDSTCTCPGPGYKNCSPVSRCE 420
Db |||||
QY 421 HPCNGATCHRRYCECAGYGGNCQFLLPEPPGVDEEQPMWVACGLVLLLLGCAAVVCV 480
QY 481 RLKQKPECETETMNNLANCQREKDSISGATQIKNTNKKDFHDKKRYPYVDYNLVLKHKK 540
Db |||||
QY 541 CSEKALRRKPSVYSTKDYQSVVSEKDECIATEV 578
Db |||||

RESULT 2

US-09-908-322-13

; Sequence 13, Application US/09908322

; Patent No. 6783956

GENERAL INFORMATION:

APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,322

FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mierock, S Leellie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 578 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-908-322-13

Query Match 100.0%; Score 3383; DB 4; Length 578;

Best Local Similarity 100.0%; Pred. No. 3.3e-245;

Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRLLASALLCVSGVFELKQLQEFVNKGLLRNCRGGGCTFFRVCLKHQYQASVSPPEP 60

Db |||||

QY 61 CTYGSATPVLSGSPDGAGDPAFSNPIRPFPGTWPFTSLIEALHTDSPDALTENPER 120

Db |||||

QY 121 LISRLTORHLVGEWSQDLHSSGRTDLYSYRFVCDDEHYHGECSVFCRPRDDFGHFTCCR 180

Db |||||

QY 181 GSKCPGWKQYCTPICLPGCDQHGCDKPECKCRVGMQGRYDCECIRYPCGVHGTCCQPM 240

Db |||||

QY 241 QCNQCEGWSGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSRPGYTGCBEPCCKNGS 300

Db |||||

QY 301 CTDLESSCTCPGFGYKCELSAMTADGFCFNGRCNDPDDGYYCCPLGSGFNCCKDCSS 360

Db |||||

QY 361 PCNGACVDLGNSSYCCQAGFGRCNDVDDCASPCNGGTCDVNDSTCTCPGPGYKNCSPVSRCE 420

Db |||||

QY 421 HPCNGATCHRRYCECAGYGGNCQFLLPEPPGVDEEQPMWVACGLVLLLLGCAAVVCV 480

Db |||||

QY 481 RLKQKPECETETMNNLANCQREKDSISGATQIKNTNKKDFHDKKRYPYVDYNLVLKHKK 540

Db |||||

QY 541 CSEKALRRKPSVYSTKDYQSVVSEKDECIATEV 578

Db |||||

RESULT 3

US-08-981-392-2

; Sequence 2, Application US/08981392

; Patent No. 6262025

GENERAL INFORMATION:

APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-392-2

Query Match 73.6%; Score 2489; DB 3; Length 728;
Best Local Similarity 76.0%; Pred. No. 3.4e-178;
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

Qy 5 LASALLC-----VSGVFELKLOEFVNKKGLL-NRNCRRGGG-----CCTFFRVCL 48
Db 11 LLSALLCRCQVDSGVFELKLOEFVNKKGLLSNRNCRGGGGAGGQCCDCKTFFRVCL 70

Qy 49 KHYQASVSPPECTYGS--TPVLG--SPS-PDGAG--DPATSNPIRPFPGTWPCTSLI 102
Db 71 KHYQASVSPPECTYGSAITPVLGANSFSVDPGAGADPAFNPPIRPFPGTWPCTSLI 130

Qy 103 IEALHTSPDDL-TENPERLISRL-TQRHL-VGEWSDQLHSSGRTDL-YSYRFVCDHY 158
Db 131 IEALHTSPDDLTTENPERLISRLATQRHLAVGEWSDQLHSSGRTDLKYSYRFVCDHY 190

Qy 159 YGEGCSVFCRRDD-FGHFTCG-RGEK-C-PGWGQYCT-PICLPQCD-QHG-CDKPGEC 211
Db 191 YGEGCSVFCRRDDRFHFTCGRGEKVCNPGWQYCTETICLPQCDQHGCDKPGEC 250

Qy 212 KCRVGMQRYCDEIRYPCGVHGTCCQPWQCNCQEGWGLFCNQDNLNCTHHKPC-NGAT 270
Db 251 KCRVGMQRYCDEIRYPCGVHGTCCQPWQCNCQEGWGLFCNQDNLNCTHHKPC-KNGAT 310

Qy 271 CTNTGQGSYTCSCRPGYTG--CE---BEC---PCKN-GSCTDLSE--SCTCPPGFYGK-C 318
Db 311 CTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGSGCTDLSENSCTCPPGFYGKNC 370

Qy 319 ELSAMTCADGCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
Db 371 ELSAMTCADGCFNGRCRTDNPDGGYSCRCPLGSGFNCEKKIDYCSSSPCANGACVDL 430

Qy 370 GNSY-C-COAGF-GR-C-DNVDCCAS-PC-NGGTC-D--VND-SCTCPPGY-GKNCS-PVS 417
Db 431 GNSYICQCAQGTGRHCDNDVDCCASPCVNGGTCCQDGVNDYCTCPPGYNGKNCSTPVS 490

Qy 418 RCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLPLPEPP-GPV-----DBEQ 458

Db 491 RCEHPCHNGATCHERSNRYVCECARGYGLNCOFLPEPPQGPVIVDFTBKYTEGONSQ 550
Qy 459 FPM-AVCAGLVL---LLLGCAA-VVCVRLK-----QKPEC---ETETMNNLANCOREKD- 504
Db 551 FPMIACAGIILVLMLLGCAAIVVCVRLKVQKHHQFPCARSETETMNNLANCOREKDI 610
Qy 505 --SSIGATQIKNTKK-DFH-----DK---KVRYP-VDYNLVLKV-----HKKC--- 541
Db 611 SISVIGATQIKNTKKVDHSDNSDKNGYKVRYPSVDYNLVELKNEPSVKEEHGKCEAK 670
Qy 542 -----SEKAL-----RKRP-SYVTSKOTKYQSVYV--SEKDESC-IATEV 578
Db 671 CETYDSEAEKSAVOLKSSDTSERKRPDSVYSTKDTKYQSVYVISEEKDECIATEV 728

RESULT 4
US-09-908-322-2
; Sequence 2, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-908-322-2

Query Match 73.6%; Score 2489; DB 4; Length 728;
Best Local Similarity 76.0%; Pred. No. 3.4e-178;
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

Qy 5 LASALLC-----VSGVFELKLOEFVNKKGLL-NRNCRRGGG-----CCTFFRVCL 48
Db 11 LLSALLCRCQVDSGVFELKLOEFVNKKGLLSNRNCRGGGGAGGQCCDCKTFFRVCL 70

Qy	49	KHYQASVSPPEPCTYGS-A-TPVLG--SPS-PDGAG--DPAFSNP	IRPPFGFTWPGTFSLI	102	
Db	71	KHYQASVSPPEPCTYGS-AITPVLGANSFSVPDGAGADPAFSNP	IRPPFGFTWPGTFSLI	130	
Qy	103	IBALHTSDSDLL-TENPERLLSR-L-TORHL--VGREMSODLHSSGRD	L--YSYRFVUCDEHY	158	
Db	131	IBALHTSDSDLLTTENPERLLSR-LATQRHLAVGREMSODLHSSGRD	LKYSYRFVUCDEHY	190	
Qy	159	YEGGCVFCRPRDD--FGHFTCG-RBEK-C-PGWKGQYCT-PICLP	PGCD-OHG-CDKPGBC	211	
Db	191	YEGGCVFCRPRDDRGHFTCGERGEKVCNPGWKGQYCTBPICLP	PGDEQHGFCDXPGBC	250	
Qy	212	KCRVGNQGRYCDCECIYPCGVHGTCCQPWQCNCOEGHGLFCNQD	LNLYCTHHKPC--NGAT	270	
Db	251	KCRVGNQGRYCDCECIYPCGLHGTCCQPWQCNCOEGHGLFCNQD	LNLYCTHHKPCNGAT	310	
Qy	271	CTNTGGSYTSCRPGYTG--CE---BEC---PCN-GSCTDL	ES--SCTCPPGFYGK-C	318	
Db	311	CTNTGGSYTSCRPGYTGSSCEIENECDANPCKNGGSCCTDL	ENSYSCTCPPGFYGKNC	370	
Qy	319	ELSAMTCADPCFNGRC-DNPDGGY-C-CPLG-SGFENCEK	--DCSSSPC-NGA-CVDL	369	
Db	371	ELSAMTCADPCFNGRCTDNPDGGYSCRPLGYSGFENCEK	KIDYCSSSPCANGAQCVDL	430	
Qy	370	GNSY-C-COAGF-GR-C-DNVDDCAS-PC-NGGTC	D--VND-SCTCPPGY-GKNC	PVS	417
Db	431	GNSYTCQCAQFTGRHCDNVDDCASFPVNGGTCQDGVNDY	SCTCPPGYNGRNCSTPVS	490	
Qy	418	RCHE-PCHNGATCHRR---CECA-GYGG-NCOFLLPEPP	-GPV-----DEEQ	458	
Db	491	REHNPCNGATCHERSNRYCECARGVGLNCOFLLPEPP	GPVIVDFTEKYTEQNSQ	550	
Qy	459	FPW-AVCAGLVL---LLIGCAA-VVVRLK-----QKPEC	---ETETMNNLANCQREKD-	504	
Db	551	FPWIAVCAGIILVLLMLLGCAIIVCVRLKVKQRHHQPEACR	SETETMNNLANCQREKDI	610	
Qy	505	---SSIGATQIKNTNKK-DPH---DK---KVRYP-VDN	YLVLK-----HKC---	541	
Db	611	SISVIGATQIKNTNKKVDFHSDNSDKYKVRYPSVDN	LVHLEKNEDSVKEHGKCEAK	670	
Qy	542	-----SEKAL-----RKRP-SVYSTSKOTKYOSVYV	---SEKDEC-IATEV	578	
Db	671	CETYDSEAEKESAVOLKSDTSERKRPDSVYSTSKOTKYOSV	VISEKDECIATEV	728	

RESULT 5

```

US-08-872-855-8
; Sequence 8, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESS: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

```


US-09-908-322-12

Query Match 72.8%; Score 2462; DB 4; Length 722;
Best Local Similarity 75.9%; Pred. No. 3.5e-176;
Matches 548; Conservative 6; Mismatches 24; Indels 144; Gaps 68;

QY 1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRG-----GCCTPFR 45
DB 1 MGRSALALAVVALLCQWSSGVFELKQEFVNKKGLLNRNCRRGSGPPCACRTPFR 60

QY 46 VCLKHQVQSVSPPECTYGS-A-TPVLG--SFS-PDGAG-DPAFSPNPIRPFPGFTWPGTFS 100
DB 61 VCLKHQVQSVSPPECTYGS-AVTPVLGVSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTFS 120

QY 101 LIIEALHTSDPDDL-TENPERLISRL-TORHL-VGEWSQDLHSSGRTDL-VSYRVFVDEB 156
DB 121 LIIEALHTSDPDDL-TENPERLISRL-TORHLTVGEWSQDLHSSGRTDLVSYRVFVDEB 180

QY 157 HYEGECVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209
DB 181 HYEGECVFCRPRDDAFGHFTCGDRGKMDPGWKQYCTDPICLPGCCDDQHGCDKPG 240

QY 210 ECKRVGMQGRYDCIRYPCGVHGTQCPWQCNCOEGWGLFCNODLNYCTHHKPC-NG 268
DB 241 ECKRVGMQGRYDCIRYPCGVHGTQCPWQCNCOEGWGLFCNODLNYCTHHKPC-NG 300

QY 269 ATCTNTGQSYTSCSRPGYTG--CE---BEC---PCKNG-SCTDLES--SCTCPPGYGK 317
DB 301 ATCTNTGQSYTSCSRPGYTGANCELEVDCAFPCKNGASCTDLEDSFSCTCPGPGYGK 360

QY 318 -CELSAMTCADGCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKDD--C-SSPC-NGA-CV 367
DB 361 VCELSAMTCADGCFNGGRCSDNPDGGYTCHCPLGSGFNCEKMDLCSGSPCSNGAKCV 420

QY 368 DLGNSY-C-CQAGF-GR-C-DNVDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415
DB 421 DLGNSYLCRCQAGFSGRYCEDNVDCA-SPCANGGTCRDSVNDFSCTCPPGYGKNCSAP 480

QY 416 VSRCEH-PCNHGATCHRR-----YCECA-GYGG-NCQFLPE-PPGP--VD-----EQ- 458
DB 481 VSRCEHAPCHGATCHQGRQYVCECAQYGGPNCQFLPEPPGPMVVDLSERHMSQG 540

QY 459 --PPW-AVCAGLV---LLLLGCAA-VVVRLLK-QK---PE-C--ETETMNNLANCOREK 503
DB 541 GPPWVAVAGVVLVLLLLGCAA-VVVRLLKQKQHPPEPPGPMVVDLSERHMSQG 600

QY 504 D-----SSIGATQIKNTKK-DFHDK-----KVRYP-VDYNLV-----LK 536
DB 601 DVSVSLIGATQIKNTKKADFGDHGAESKSFVRYPTVDYNLVRLDKGEATVRDTHSK 660

QY 537 VHKKEEVALRKR-----PSVYSTKDTKYQSVYV--SEKDEC-IAT 576
DB 661 RDTKQSQSLQEKRRSPQHLVGVRFLTENRPSVYSTKDTKYQSVYVLSAEKDECVIAT 720

QY 577 EV 578
DB 721 EV 722

RESULT 8

US-08-872-855-4
; Sequence 4, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
LENGTH: 720 amino acids
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-855-4

Query Match 72.5%; Score 2454; DB 3; Length 720;
Best Local Similarity 76.4%; Pred. No. 1.4e-175;
Matches 551; Conservative 6; Mismatches 20; Indels 144; Gaps 71;

QY 1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRG-----GCCTPFR 45
DB 1 MGRSALALAVVALLCQWSSGVFELKQEFVNKKGLLNRNCRRGSGPPCACRTPFR 60

QY 46 VCLKHQVQSVSPPECTYGS-A-TPVLG--SFS-PDGAG-DPAFSPNPIRPFPGFTWPGTFS 100
DB 61 VCLKH-QASVSPPECTYGS-AVTPVLGVSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTFS 119

QY 101 LIIEALHTSDPDDL-TENPERLISRL-TORHLVGEWSQDLHSSGRTDL-VSYRVFVDEB 157
DB 120 LIIEALHTSDPDDL-TENPERLISRL-TORHLTVGEWSQDLHSSGRTDLVSYRVFVDEB 179

QY 158 YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 210
DB 180 YGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKQYCTDPICLPGCCDDQHGCDKPG 239

QY 211 CKCRVGMQGRYDCIRYPCGVHGTQCPWQCNCOEGWGLFCNODLNYCTHHKPC-NGA 269
DB 240 CKCRVGMQGRYDCIRYPCGVHGTQCPWQCNCOEGWGLFCNODLNYCTHHKPC-NGA 299

QY 270 TCTNTGQSYTSCSRPGYTG--CE---BEC---PCKNG-SCTDLES--SCTCPPGYGK- 317
DB 300 TCTNTGQSYTSCSRPGYTGANCELEVDCAFPCKNGASCTDLEDSFSCTCPGPGYGV 359

QY 318 CELSAMTCADGCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKDD--C-SSPC-NGA-CVD 368
DB 360 CELSAMTCADGCFNGGRCSDNPDGGYTCHCPLGSGFNCEKMDLCSGSPCSNGAKCV 419

QY 369 LGNSY-C-CQAGF-GR-C-DNVDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PV 416
DB 420 LGNSYLCRCQAGFSGRYCEDNVDCA-SPCANGGTCRDSVNDFSCTCPPGYGKNCSAPV 479

QY 417 SRCEH-PCNHGATCHRR-----YCECA-GYGG-NCQFLPE-PPGP--VD-----EQ- 458
DB 480 SRCEHAPCHGATCHQGRQYVCECAQYGGPNCQFLPEPPGPMVVDLSERHMSQG 539

QY 459 --PPW-AVCAGLV---LLLLGCAA-VVVRLLK-QK---PE-C--ETETMNNLANCOREK 504
DB 540 PPPWVAVAGVVLVLLLLGCAA-VVVRLLKQKQHPPEPPGPMVVDLSERHMSQG 599

QY 505 ---SSIGATQIKNTKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK- 540

Db 600 VSVSIIIGATQKNTNKKADFGDHGAKKSFKRYPTVDYNLVRDLKGDEATVRDTHSKR 659
Qy 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IATE 577
Db 660 DTKQSQSSAGEEKIAPTLRGEIPDRKRPSVYSTSKDTKYQSVVLSAEKDECVIATE 719
Qy 578 V 578
Db 720 V 720
RESULT 9
US-08-872-855-5
; Sequence 5, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-872-855-5
Query Match 72.3%; Score 2447.5; DB 3; Length 713;
Best Local Similarity 75.7%; Pred. No. 4.2e-175;
Matches 540; Conservative 9; Mismatches 29; Indels 135; Gaps 66;
Qy 1 MGR-----LLASALLC---VSGVFELKLOEFVNKKGLL-NRNCRRGG-----CCCTFFR 45
Db 1 MGRSALALAVSALLCQVSSGVFELKLOEFVNKKGLLNRCRRGGSGPPCACRTFFR 60
Qy 46 VCLKHYQASVSPPECTYVGS-TPVLG--SFS-PDGAG-DPAFNPFRFPFGFTWPGTFS 100
Db 61 VCLKHYQASVSPPECTYVGSATVAVLGVDSFSLPDGAGIDPAFNPFRFPFGFTWPGTFS 120
Qy 101 LIIEALHTSDPDL-TENPERLISRL-TQRHLVGEWSQDLHSSGRTDL-YSYRFVCDHE 157
Db 121 LIIEALHTSDPDLATENPERLISRLTQRHTVGEWSQDLHSSGRTDLYSYRFVCDHE 180
Qy 158 YYGEGCSVFCPRDD-FGHFTCG-RGEK-C-PGHWGOYCT-PICLPGC-DOHG-CDKPG 210
Db 181 YYGEGCSVFCPRDDAFGHFTCGRGEKMWCDPGWKQYCTDPICLPGCDDQHGCDKPG 240

Qy 211 CKRVGMQGRYCDCEIRYPCGVHGTCCQPMQCNQCEGWGLFCNQDLYNCTHHKPC-NGA 269
Db 241 CKRVGMQGRYCDCEIRYPCGLHGTCCQPMQCNQCEGWGLFCNQDLYNCTHHKPC-NGA 300
Qy 270 TCTNTGQSVYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES---SCTCPPGFYK- 317
Db 301 TCTNTGQSVYTCSCRPGYTGANCELEVDCAPEPCNKGSGCTDLEDYSCTCPPGFYKV 360
Qy 318 CELSAMTCADGPCFNGGRC-DNPDGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVD 368
Db 361 CELSAMTCADGPCFNGGRCSDNPDGYTCHCPAGSGFNCEKKIDLCSSSPCSNGAKCVD 420
Qy 369 LGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PV 416
Db 421 LGNSYLCRCQCTGFSGRYCEDNVDDCASSPCANGGTCDSDVDFCTCPPGYTGKNCSAPV 480
Qy 417 SRCEH-PCNGATCHRR-----YCECA-GYGG-NCQFLLPEPPGPV---DEEQPW-AVC 464
Db 481 SRCEHAPCHNGATCHQRQRYMCECAQGYGGANCOFLLPEPPDLIVAAQGSFPWAVC 540
Qy 465 AGLV---LLLLGCAA-VVCURLK---QKP--EC--ETETMNNLANCOREKD---SSIGA 509
Db 541 AGVVLVLLLLGCAA-VVCURLKQKHQPPDPCGGGTETMNNLANCOREKDVSVSIIGA 600
Qy 510 TQIKNTNKK-DFH-----DK---KVRYP-VDYNLV--LK-----VHKK----- 540
Db 601 TQIKNTNKKADFGDHGADKSSFKARYPTVDYNLIRDLKGDEATVRDAHSKRDTKCQSQG 660
Qy 541 -CSEKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578
Db 661 SAGEKSTSTLRGGEVDPDRKRPSVYSTSKDTKYQSVVLSAEKDECVIATEV 713

RESULT 10

US-09-068-740A-9
; Sequence 9, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR FILING DATE: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-068-740A-9

Query Match 71.0%; Score 2401.5; DB 3; Length 723;
Best Local Similarity 75.1%; Pred. No. 1.2e-171;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;
Qy 7 SALLC---VSGVFELKLOEFVNKKGLL-NRNCRRGG-----GCCTFRVCLKHQASVS 56
Db 13 SALLCQVSSGVFELKLOEFVNKKGLLNRCRRGGAGPPCACRTTFRVCLKHQASVS 72
Qy 57 PEPPTCYGSA-TPVLG--SFS-PDGAG-DPAFNPFRFPFGFTWPGTFSIIIEALHTDSP 111
Db 73 PEPPTCYGSAVTPVLGVDSFSLPDGAGADSAFNPFRFPFGFTWPGTFSIIIEALHTDSP 132
Qy 112 DDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHEHYGEGCSVFC 167

Db 133 DDLATENPERLISRLATQRHLTVGEWSDQLHSSGRTDLKYSYRVCDEHHYEGGCSVFC 192
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPQCD-QHG-CDKPGCKRCRVGWQGR 220
Db 193 RPRDDAFGHFTGGERGEKVCNPGWKGPYCTETPICLPQCDQHGFCDKPGCKRCRVGWQGR 252
QY 221 YDECIIRYPCGVHGTCCQPPWQCNQCBGGLFCNODLNYCTHHKPC-NGATCTNTGQGSY 279
Db 253 YDECIIRYPCGLHGTCCQPPWQCNQCBGGLFCNODLNYCTHHKPCNKGATCTNTGQGSY 312
QY 280 TCSRPGYTG--CE---BEC---PCKN-GSCDTLES--SCTCPPGFGYK-CBLSAMTCAD 327
Db 313 TCSRPGYTGATCELIGIDECSPCKNGSGCTDLENSYSCTCPPGFGYKICBLSAMTCAD 372
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYS-C-CQ 376
Db 373 GPCFNGGRCSDPDGGYSCRCFVGYSGFNCEKKIDYCSSSPCSNGAKCVDLDGAYLCRCQ 432
QY 377 AGF-GR-C-DNVDCA-SPC-NGGTC--DVND-SCTCPGPGY-GKNC-PVSRCEH-PCHN 425
Db 433 AGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFCTCPGPGYTGRCNSAPVSRCEHAPCHN 492
QY 426 GATCHRR----YCECA-GYGG-NCQFLPPE-PPGP--VD-----BEQ----FPW-AVCAGL 467
Db 493 GATCHERHRYVCECARGYGGPNCQFLLPPEPPAVVDLTKLEGQGGFFPFWAVCAGV 552
QY 468 VL---LLLGCAA-VVVCRL---KQKPEC-----ETETMNNLANCQREKD---SSIGATQI 512
Db 553 ILVLMLLGCAAVVVCRLQLQKRRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612
QY 513 KNTNKK-DPH-----DK---KVRYP-VDYNLV-----LKVHKK-----S 542
Db 613 KNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTCQPGSSG 672
QY 543 EBKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578
Db 673 BEKGPTTLRGGEASERKRPDSCSTSKDTKYQSVVISEEKDECVIATEV 723

RESULT 11

US-09-423-753-27

; Sequence 27, Application US/09423753

; Patent No. 6664098

; GENERAL INFORMATION:

; APPLICANT: SAKANO, SEIJI

; TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR

; FILE REFERENCE: KP-8693

; CURRENT APPLICATION NUMBER: US/09/423,753

; CURRENT FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: PCT/JP98/02104

; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: JP 9/124064

; PRIOR FILING DATE: 1997-05-14

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 27

; LENGTH: 723

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-423-753-27

Query Match

Best Local Similarity 71.0%; Score 2401.5; DB 4; Length 723;

Matches 534; Conservativity 75.1%; Pred. No. 1.2e-171;

Matches 534; Conservativity 11; Mismatches 27; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFELKQFVFNKGLL--NRNCRGG-----GCCTFFRVCLKHQASVS 56

Db 13 SALLCQVWSSGVFELKQFVFNKGLLGNRCRGAGPPACRTFFRVCLKHQASVS 72

QY 57 PEPPTCTYGA-TPVLG--SFS-PDGAG-DPAFSNPTRPFGTWTGTFSLIIEALHTDSP 111

Db 73 PEPPTCTYGA-TPVLGVSFSLPDGGGADSAFNPTRPFGTWTGTFSLIIEALHTDSP 132

QY 112 DDL-TENPERLISRL-TORHL-VGEWSDQLHSSGRTDL-YSYRVCDEHHYEGGCSVFC 167
Db 133 DDLATENPERLISRLATQRHLTVGEWSDQLHSSGRTDLKYSYRVCDEHHYEGGCSVFC 192
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPQCD-QHG-CDKPGCKRCRVGWQGR 220
Db 193 RPRDDAFGHFTGGERGEKVCNPGWKGPYCTETPICLPQCDQHGFCDKPGCKRCRVGWQGR 252
QY 221 YDECIIRYPCGVHGTCCQPPWQCNQCBGGLFCNODLNYCTHHKPC-NGATCTNTGQGSY 279
Db 253 YDECIIRYPCGLHGTCCQPPWQCNQCBGGLFCNODLNYCTHHKPCNKGATCTNTGQGSY 312
QY 280 TCSRPGYTG--CE---BEC---PCKN-GSCDTLES--SCTCPPGFGYK-CBLSAMTCAD 327
Db 313 TCSRPGYTGATCELIGIDECSPCKNGSGCTDLENSYSCTCPPGFGYKICBLSAMTCAD 372
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYS-C-CQ 376
Db 373 GPCFNGGRCSDPDGGYSCRCFVGYSGFNCEKKIDYCSSSPCSNGAKCVDLDGAYLCRCQ 432
QY 377 AGF-GR-C-DNVDCA-SPC-NGGTC--DVND-SCTCPGPGY-GKNC-PVSRCEH-PCHN 425
Db 433 AGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFCTCPGPGYTGRCNSAPVSRCEHAPCHN 492
QY 426 GATCHRR----YCECA-GYGG-NCQFLPPE-PPGP--VD-----BEQ----FPW-AVCAGL 467
Db 493 GATCHERHRYVCECARGYGGPNCQFLLPPEPPAVVDLTKLEGQGGFFPFWAVCAGV 552
QY 468 VL---LLLGCAA-VVVCRL---KQKPEC-----ETETMNNLANCQREKD---SSIGATQI 512
Db 553 ILVLMLLGCAAVVVCRLQLQKRRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612
QY 513 KNTNKK-DPH-----DK---KVRYP-VDYNLV-----LKVHKK-----S 542
Db 613 KNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTCQPGSSG 672
QY 543 EBKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578
Db 673 BEKGPTTLRGGEASERKRPDSCSTSKDTKYQSVVISEEKDECVIATEV 723

RESULT 12

US-10-140-002-346

; Sequence 346, Application US/10140002

; Patent No. 6725730

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330RIC59

; CURRENT APPLICATION NUMBER: US/10/140,002

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 346

; LENGTH: 723

; TYPE: PRT


```
; ORGANISM: Homo Sapien
US-10-140-002-346

Query Match
  71.0%; Score 2401.5; DB 4; Length 723;
  75.1%; Pred. No. 1.2e-171;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

Qy 7 SALLC---VSGVFELKQEFVKKGLL-NRNCRRGG-----GCCTFFRVCLKHQASVS 56
Db 13 SALLCQVSSGVFELKQEFVKKGLLNRNCRRGGAGPPCACRTFFRVCLKHQASVS 72
Qy 57 PEPCCTYCSA-TPVLG--SFS-PDGAG-DPAFSPNIRFPFGFTWPGTFSLLIEALHTDSP 111
Db 73 PEPCCTYCSAVTPVLGVSFSLPDGGGADSAFSPNIRFPFGFTWPGTFSLLIEALHTDSP 132
Qy 112 DDL-TEMPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHYHYGGCVFC 167
Db 133 DDLATEPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDHYHYGGCVFC 192
Qy 168 RPRDD-FGHFTCG-RGEK-C-PGKQGYCT-PICLPGCD-QHG-CDKPGCKCRVGMQGR 220
Db 193 RPRDDAFGHFTCGERGEKVCNPGKGPYCTEPICLPGCDEQHGFCDEKPGCKCRVGMQGR 252
Qy 221 YDCSIRYPGCVHGTCCQPMQCNQCEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279
Db 253 YDCSIRYPGCLHGTCCQPMQCNQCEGWGGLFCNQDLNYCTHHKPCNKGATCTNTGQGSY 312
Qy 280 TCSCRPGVTG--CE---EEC---PCKN-GSCTDLES--SCTCPGPGYVK-CELSAMTCAD 327
Db 313 TCSCRPGYTGATCELGIDECDPSPCKNGSGCTDLENSYSCTCPGPGYVKICELSAMTCAD 372
Qy 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYSY-C-CQ 376
Db 373 GPCFNGGRCSDPDGGYSCRCPCVYSGFNCEKKIDYCSGSPCSNGAKCVDLGDALCRQ 432
Qy 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPGPGY-GKNCS-PVSRCEH-PCHN 425
Db 433 AGFSGRCHDDNVDDCASSPCANGGTCRDGVNDFSCCTPPGYTGRNCSAPVSRCEHAPCHN 492
Qy 426 GATCHRR---YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPM-AVCAGL 467
Db 493 GATCHERHRYVCBARGYGGPNQFLLPELPPGPAVDLTKLEGGGGPPFWAVACGV 552
Qy 468 VL---LLLGCAA-VVCVRL---KQPEC-----ETETMNNLANCQREK---SSIGATQI 512
Db 553 ILVLMLLGCAAVVVCVRLRLQKRRPADPCRGETETMNNLANCQREKDISVSIIGATQI 612
Qy 513 KNTNKK-DHF-----DK---KVRYP-VDYNLV-----LKVHKK-----S 542
Db 613 KNTNKKADFHDHSAKNGFKARYPAVDYNLVQDLKGDPTAVRDAHSKRDTCQPGQSSG 672
Qy 543 EEKAL-----RERP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578
Db 673 EEKGTPTLGGEASERKRPDSCGCTSKDTKYQSVVISEEKDECVIATEV 723

RESULT 13
US-09-068-740A-4
; Sequence 4, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068, 740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15

; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-068-740A-4

Query Match
  70.6%; Score 2390; DB 3; Length 702;
  75.4%; Pred. No. 8.2e-171;
Matches 529; Conservative 11; Mismatches 26; Indels 136; Gaps 66;

Qy 13 SGVFELKQEFVKKGLL-NRNCRRGG-----GCCTFFRVCLKHQASVSPEPCTYGS 65
Db 1 SGVFELKQEFVKKGLLNRNCRRGGAGPPCACRTFFRVCLKHQASVSPEPCTYGS 60
Qy 66 A-TPVLG--SFS-PDGAG-DPAFSPNIRFPFGFTWPGTFSLLIEALHTDSDDDL-TEMP 119
Db 61 AVTPVLGVDSFSLPDGGGADSAFSPNIRFPFGFTWPGTFSLLIEALHTDSDDDLATENPE 120
Qy 120 RLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHYHYGGCVFCRPRDD-FGH 175
Db 121 RLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDHYHYGGCVFCRPRDDAFGH 180
Qy 176 FTCG-RGEK-C-PGKQGYCT-PICLPGCD-QHG-CDKPGCKCRVGMQGRYDCIRYP 229
Db 181 FTCGERGEKVCNPGKGPYCTEPICLPGCDEQHGFCDEKPGCKCRVGMQGRYDCIRYP 240
Qy 230 GCVHGTCCQPMQCNQCEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCRPGYT 288
Db 241 GCLHGTCCQPMQCNQCEGWGGLFCNQDLNYCTHHKPCNKGATCTNTGQGSYTCSCRPGYT 300
Qy 289 G--CE---EEC---PCKN-GSCTDLES--SCTCPGPGYVK-CELSAMTCADGPGFNGGRC 336
Db 301 GATCELGIDECDPSPCKNGSGCTDLENSYSCTCPGPGYVKICELSAMTCADGPGFNGGRC 360
Qy 337 -DNPDGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYSY-C-CQAGF-GR-C- 382
Db 361 SDSPDGGYSCRCPCVYSGFNCEKKIDYCSGSPCSNGAKCVDLGDALCRQAGFSGRHCD 420
Qy 383 DNVDDCA-SPC-NGGTC--DVND-SCTCPGPGY-GKNCS-PVSRCEH-PCHNGATCHRR-- 432
Db 421 DNVDDCASSPCANGGTCRDGVNDFSCCTPPGYTGRNCSAPVSRCEHAPCHNGATCHERGH 480
Qy 433 --YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPM-AVCAGLVL---LLLG 473
Db 481 RYVCECARGYGGPNQFLLPELPPGPAVDLTKLEGGGGPPFWAVACAGVILVLMLLLG 540
Qy 474 CAA-VVCVRL---KQPEC-----ETETMNNLANCQREK---SSIGATQIKNTNKK-DP 520
Db 541 CAAVVCVRLRLQKRRPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADF 600
Qy 521 H-----DK---KVRYP-VDYNLV-----LKVHKK-----SEKAL----- 547
Db 601 HGDHSAKNGFKARYPAVDYNLVQDLKGDPTAVRDAHSKRDTCQPGQSSGSEKGTPTTL 660
Qy 548 -----RERP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578
Db 661 RGGEASERKRPDSCGCTSKDTKYQSVVISEEKDECVIATEV 702

RESULT 14
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 2001.30.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-6

Query Match      70.4%; Score 2380.5; DB 4; Length 723;
Best Local Similarity 74.7%; Pred. No. 4.4e-170;
Matches 531; Conservative 11; Mismatches 30; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFELKQLQFVNKKGLL-NRNCRRGG-----GCCTFFRVCLKHQAQSVS 56
DB 13 SALLCQVSSGVFELKQLQFVNKKGLLGNPCRRGGAGPPACACRTFFRVCLKHQAQSVS 72
QY 57 PEPPCTYGSA--TPVLG--SFS--PDGAG-DPAFNSPIRPFPGFTWPGTFFSLIIEALHTDSP 111
DB 73 PEPPCTYGSVAVTVLGVDSFSLPDGGGADSAFNSPIRPFPGFTWPGTFFSLIIEALHTDSP 132
QY 112 DDL-TENPERLISRL--TORHL-VGEESODLHSSGRTDL-VSYRFVCDDEHYHGGCSVFC 167
DB 133 DDLATENPERLISPLATQRLHTLVGEESQDLHSSGRTDLKYSYRFVCDDEHYHGGCSVFC 192
QY 168 RPRDD--FGHFTCG-RGEK-C-PGWKGQYCT-PICLPQCD-QHG-CDKPGCKRCRVGMQGR 220
DB 193 RPRDDAFGHFTCGERKEVCNPGWKGPYCTEPICLPQCDQHGFCQKPGCKRCRVGMQGR 252
QY 221 YDECIIRYGCYVHGTCCQWQCNCQBGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279
DB 253 YDECIIRYPCGLHGTCCQWQCNCQBGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY 312
QY 280 TCSCRPGYTG--CE---EBC---PCKN-GSCTDLES--SCTCPPPGFYGK-CELSAMTCAD 327
DB 313 TCSCRPGYTGATCELGIDECDSPPCKNGSGCSDLNYSCTCPPGYGKICLSAMTCAD 372
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYSY-C-CQ 376
DB 373 GPCFNGGRCSDPDGGYSRCPCVGYSGFNCEKKIDYCSSSPCSNCAKCVLDGAYLCRCQ 432
QY 377 AGF-GR-C-DNVDDCA-SFC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCNH 425
DB 433 AGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSTCTCPPGYTGRNCSAPVSRCEHAPCHN 492
QY 426 GATCHRR---YCECA-GYGG-NQCFLLPE-PPGP--VD---EQ---EQQ---FPW-AVCAGL 467
DB 493 GATCHERGHYVCECARGYGGNCQFLPELPPGPAVDLTTEKLEGGQGGFFPWAVACGV 552
QY 468 VL---LLLGCAA-VVCVRL---KQKPEC-----ETETMNNLANCQREK---SSIGATQI 512
DB 553 ILVLMLLGCAAVVVCVPLRLQKRPADPCRGETETMNNLANCQREKDISVSIIGATQI 612
QY 513 KNTNKK-DFH-----DK---KVRYP-VDNVLV-----LKVHKKC-----S 542
DB 613 KNTNKKADPHGDSADKNGFKARYPAVDYLVQDLKGDPTAVRDAHSKRDTKCPQGGSSG 672
QY 543 BEKAL-----RKRP-SVYSTSCKTKYQSVV--SEKDEC-IATEV 578
DB 673 BEKGTPTLURGEASERKRPDSCGCTSKOTKYQSVYVISEEKDECVIATEV 723

RESULT 15
US-08-981-392-5
; Sequence 5, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Atavanis-Teakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:

; ADDRESSER: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-5

Query Match      66.9%; Score 2262.5; DB 3; Length 721;
Best Local Similarity 68.7%; Pred. No. 2.9e-161;
Matches 489; Conservative 39; Mismatches 47; Indels 137; Gaps 61;

QY 4 LLASALLC---VSGVFELKQLQFVNKKGLL-NRNCRRGG-----CCTFFRVCLKHV 51
DB 10 LVLSAVLQICSGLFEIQLQFVNKKGLLGNMNCRRPGSLASLQRCCEKCTFFRICKHY 69
QY 52 QASVSEPPCTYGSA--TPVLGSFS---PDGA-GDPAFNSPIRPFPGFTWPGTFFSLIIEAL 106
DB 70 QSNVSEPPCTYGGAVTVLGTNSFWVPSSNADPTFSNPIRPFPGFTWPGTFFSLIIEAI 129
QY 107 HTDSRDDL-TENPERLISRL--TORHL-VGEESODLHSSGRTDL-VSYRFVCDDEHYHGG 162
DB 130 HADSADDLNTENPERLISRLATQRLHTLVGEESQDLHSSDRTELKYSYRFVCDDEHYHGG 189
QY 163 CSVFCRPRDD--FGHFTCG-RGEK-C-PGWKGQYCT-PICLPQCDQHG--CDKPGCKRCV 215
DB 190 CSDYCRPRDDAFGHFSCEKGEKLCNPGWKGLYCTEPICLPQCDDEHHGYCDKPGCKRCV 249
QY 216 GWQGYCDECIIRYGCYVHGTCCQWQCNCQBGWGLFCNQDLNYCTHHKPC-NGATCTNT 274
DB 250 GWQGYCDECIIRYPCGLHGTCCQWQCNCQBGWGLFCNQDLNYCTHHKPCNGATCTNT 309
QY 275 GQGSYTCSCRPGYTG--CE---EBC---PCKN-GSCTDLES--CTCPPGYGK-CELSA 322
DB 310 GQGSYTCSCRPGYTGSCNCEIEVNECDAMPCKNGSGCSDLNYSCTCPPGYGKNCLESA 369
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DB 370 MTCADGPCFNGGRCADNDPDGGYICFPVGYSGFNCEKKIDYCSSNPGANGARCEDLGNYSY 429
QY 374 CQQA--GF-GR-C-DNVDDCAS-PC-NGGTCB--VND-SCTCPPGY-GKNCS-PVSRCEH 421
DB 430 ICQCQEGFSGRNCDNLDDBCTSPQNGGTCQDQINDYSCTCPGGYIGKNCSMPITKCEH 489
QY 422 -PCHNGATCHRR-----YCECA-GYGG-NQCFLLP-EPPGPVD-----BEQFPW-AV 463
DB 490 NPECHNGATCHERNRYVCCARGYGNNCQFLPEKPVVVDLTTEKYTEGGQGGQFPWIAV 549
QY 464 CAGLVL---LLLGCAA-VVCVRL-----KQKPEC-----ETETMNNLANCQREK---SSIG 508
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Search completed: November 29, 2004, 13:28:07
Job time : 19.1897 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:26:20 ; Search time 58.226 Seconds
(without alignments)
3520.994 Million cell updates/sec

Title: US-09-783-931-13

Perfect score: 3383

Sequence: 1 MGRLLASALLCVSGVFELK.....DTKQSVYVSEKDECIATEV 578

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3383	100.0	578 10	US-09-783-931-13
3	2489	73.6	728 9	US-09-908-322-2
4	2489	73.6	728 10	US-09-783-931-2
5	2488.5	73.6	729 14	US-10-417-719-8
6	2466	72.9	722 15	US-10-042-865-107
7	2466	72.9	722 16	US-10-731-741-4
8	2462	72.8	722 9	US-09-908-322-12
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45	2401.5	71.0	723 14	US-10-140-925-346

ALIGNMENTS

RESULT 1

Sequence 13, Application US/09908322

Patent No. US20020107194A1

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,322

FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-908-322-13

Query Match 100.0%; Score 3383; DB 9; Length 578;
Best Local Similarity 100.0%; Pred. No. 3e-238;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGRLLASALLCVSGVFELKQLQEFVNKGLLNRCRCGGCCCTFFRVCLAKHYQASVSPPEP 60

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DB 61 CTYGSATPVLSGSPDGADPAFNSPIRPFPGFTWPGTFSLLIEALHTDSPDILTENPER 120

QY 121 LISRLTORHLVGEWSQDLHSSGRTDLYSYRFVCDDEHYHGGCVSFCRPRDDFGHFTCGR 180
DB 121 LISRLTORHLVGEWSQDLHSSGRTDLYSYRFVCDDEHYHGGCVSFCRPRDDFGHFTCGR 180

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DB 241 QNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSRCRPGYTGCBEPCPKNGS 300

QY 301 CTDLESSCTCPPGFYGKCELSAMTADGFCFNGRCNDPDGGYCCPLGSGFNCCKDCSS 360
DB 301 CTDLESSCTCPPGFYGKCELSAMTADGFCFNGRCNDPDGGYCCPLGSGFNCCKDCSS 360

QY 361 PCNGACVDLGNSSYCCQAGFGRCNDVDDCASPCNGGTCDVNDSTCTCPPGYGNKCSVSRCE 420
DB 361 PCNGACVDLGNSSYCCQAGFGRCNDVDDCASPCNGGTCDVNDSTCTCPPGYGNKCSVSRCE 420

QY 421 HPCNGATCHRRYCECAGYGGNCQFLLPEPPGPDVEEQFPMAVCAGLVLLLLGCAAVVCV 480
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RESULT 2

US-09-783-931-13
Sequence 13, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Arcavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-783-931-13

Query Match 100.0%; Score 3383; DB 10; Length 578;
Best Local Similarity 100.0%; Pred. No. 3e-238;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRLLASALLCVSGVFELKQLQEFVNKGLLNRCRCGGCCCTFFRVCLAKHYQASVSPPEP 60
DB 1 MGRLLASALLCVSGVFELKQLQEFVNKGLLNRCRCGGCCCTFFRVCLAKHYQASVSPPEP 60

QY 61 CTYGSATPVLSGSPDGADPAFNSPIRPFPGFTWPGTFSLLIEALHTDSPDILTENPER 120
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QY 121 LISRLTORHLVGEWSQDLHSSGRTDLYSYRFVCDDEHYHGGCVSFCRPRDDFGHFTCGR 180
DB 121 LISRLTORHLVGEWSQDLHSSGRTDLYSYRFVCDDEHYHGGCVSFCRPRDDFGHFTCGR 180

QY 181 GEKCPGWKQGYCTPICLPGCDQHGCDKPGCKRGMQGRYCDCEIRYPCGVHGTCCQPPW 240
DB 181 GEKCPGWKQGYCTPICLPGCDQHGCDKPGCKRGMQGRYCDCEIRYPCGVHGTCCQPPW 240

QY 241 QNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSRCRPGYTGCBEPCPKNGS 300
DB 241 QNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSRCRPGYTGCBEPCPKNGS 300

QY 301 CTDLESSCTCPPGFYGKCELSAMTADGFCFNGRCNDPDGGYCCPLGSGFNCCKDCSS 360
DB 301 CTDLESSCTCPPGFYGKCELSAMTADGFCFNGRCNDPDGGYCCPLGSGFNCCKDCSS 360

QY 361 PCNGACVDLGNSSYCCQAGFGRCNDVDDCASPCNGGTCDVNDSTCTCPPGYGNKCSVSRCE 420
DB 361 PCNGACVDLGNSSYCCQAGFGRCNDVDDCASPCNGGTCDVNDSTCTCPPGYGNKCSVSRCE 420

QY 421 HPCNGATCHRRYCECAGYGGNCQFLLPEPPGPDVEEQFPMAVCAGLVLLLLGCAAVVCV 480
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; Sequence 2, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
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; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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Qy 159 YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGMKGQYCT-PICLPGCD-QHG-CDKPGEC 211
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Qy 212 KCRVGMQGRYCDCEIRYPGCVHGTCCQFPWCNOCBEGMGLFCNQDNLNYCTHHKPC-NGAT 270
Db 251 KCRVGMQGRYCDCEIRYPGCLHGTCCQFPWCNOCBEGMGLFCNQDNLNYCTHHKPCNGAT 310
Qy 271 CTNTGQSYTCSRPYTG--CE---BEC---PCKN-GSCTDLSE--SCTCPPGFYGK-C 318
Db 311 CTNTGQSYTCSRPYTGSSCEIEINECDANPCNKGSCDTLSESYCTCPPGFYGNK 370
Qy 319 ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEBK--DSSSPC-NGA-CVDL 369
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Qy 370 GNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTC--VND-SCTCPPGY-GKNC-S-PVS 417
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US-09-783-931-2
; Sequence 2, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605

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; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-750-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-783-931-2

Query Match      73.6%; Score 2489; DB 10; Length 728;
Best Local Similarity 76.0%; Pred. No. 5.6e-173;
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

QY 5 LASALLC-----VSGVFELKLOEFVNKGLL-NRNCRRGG-----CCTFRVCL 48
Db 11 LLSALLCQVDGSGVFELKLOEFVNKGLLSNRNCRGGGAGAGQOQCDCKTFRVCL 70
QY 49 KHYQASVSEPPCTYGSA--TPVLG--SFS-PDGAG--DPAFNSPIRFPFGFTWPGTFSLI 102
Db 71 KHYQASVSEPPCTYGSAITPVLGANSFVSPDGAGGADPAFNSPIRFPFGFTWPGTFSLI 130
QY 103 IEALHTSDPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHEY 158
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QY 271 CNTNGGQYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGYGK-C 318
Db 311 CNTNGGQYTCSCRPGYTGSSCEIEINECDANPCKNNGSCTDLENSYSCTCPPGYGKNC 370
QY 319 ELSAMTCADGPCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
Db 371 ELSAMTCADGPCFNGRCCTDNPDGGYSCPLGSGFNCEKKIDYCSSPCANGAQCVDL 430
QY 370 GNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTC-D--VND-SCTCPPGY-GKNCS-PVS 417
Db 431 GNSYICQAGFGTRHCDNDVDDCASFPVNGGTCCQGVNDYSCTCPPGYGKNCSPTVS 490
QY 418 RCEH-PCHNGATCHRR-----YCECA-GYGG-NQFLLPEPP-GPV-----DEEQ 458
Db 491 RCEHNPCHNGATCHERSNRYVCECARGYGLNLCQFLLPEPPGPVIVDFTEKYTEQNSQ 550
QY 459 FFW-AVCAGLVL---LLLGCAA-VVCVRLK-----OKPEC---ETETMNNLANCOREKD- 504
Db 551 FFWIAVCAGIILVLLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNNLANCOREKDI 610
QY 505 --SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVLKV-----HKKC--- 541
Db 611 SISVIGATQIKNTNKKVDFHSDNDKNGYKVRYPVDYNLVLHKLKNEDSVKEHGKCEAK 670
QY 542 -----SEKAL-----RKRP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV 578
Db 671 CETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVYVISEKDECIATEV 728

RESULT 5
US-10-417-719-8
; Sequence 8, Application US/10417719
; Publication No. US20030180784A1
; GENERAL INFORMATION:

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; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT APPLICATION NUMBER: US/10/417,719
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 08/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Gallus Gallus
; US-10-417-719-8

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Query Match      73.6%; Score 2488.5; DB 14; Length 729;
Best Local Similarity 75.9%; Pred. No. 6.1e-173;
Matches 546; Conservative 9; Mismatches 19; Indels 145; Gaps 65;

QY 5 LASALLC-----VSGVFELKLOEFVNKGLL-NRNCRRGG-----CCTFRVCL 48
Db 11 LLSALLCQVDGSGVFELKLOEFVNKGLLSNRNCRGGGAGAGQOQCDCKTFRVCL 70
QY 49 KHYQASVSEPPCTYGSA--TPVLG--SFS-PDGAG--DPAFNSPIRFPFGFTWPGTFSLI 102
Db 71 KHYQASVSEPPCTYGSAITPVLGANSFVSPDGAGGADPAFNSPIRFPFGFTWPGTFSLI 130
QY 103 IEALHTSDPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHEY 158
Db 131 IEALHTSDPDDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLKYSYRFVCDHEY 190
QY 159 YEGGCVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPQCD-OHG-CDKPGEC 211
Db 191 YEGGCVFCRPRDDRFHFTCGERGEKVCNPGWKGOYCTEPICLPQCDQHGFCDKPGEC 250
QY 212 KCRVGHQGRYCDCEIRYPGVHGTCCQPMQCNCOEGWGLFCNQDLNYCTHHKPC-NGAT 270
Db 251 KCRVGHQGRYCDCEIRYPGCLHGTCCQPMQCNCOEGWGLFCNQDLNYCTHHKPCNGAT 310
QY 271 CNTNGGQYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGYGK-C 318
Db 311 CNTNGGQYTCSCRPGYTGSSCEIEINECDANPCKNNGSCTDLENSYSCTCPPGYGKNC 370
QY 319 ELSAMTCADGPCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NG-ACVD 368
Db 371 ELSAMTCADGPCFNGRCCTDNPDGGYSCPLGSGFNCEKKIDYCSSSPCANGAQAQVD 430
QY 369 LGNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTC-D--VND-SCTCPPGY-GKNCS-PV 416
Db 431 LGNSYICQAGFGTRHCDNDVDDCASFPVNGGTCCQGVNDYSCTCPPGYGKNCSPTV 490
QY 417 SRCEH-PCHNGATCHRR-----YCECA-GYGG-NQFLLPEPP-GPV-----DBE 457
Db 491 SRCEHNPCHNGATCHERSNRYVCECARGYGLNLCQFLLPEPPGPVIVDFTEKYTEGQNS 550
QY 458 QFPW-AVCAGLVL---LLLGCAA-VVCVRLK-----OKPEC---ETETMNNLANCOREKD 504
Db 551 QFPWIAVCAGIILVLLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNNLANCOREKD 610
QY 505 ---SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVLKV-----HKKC--- 541
Db 611 SISVIGATQIKNTNKKVDFHSDNDKNGYKVRYPVDYNLVLHKLKNEDSVKEHGKCEA 670
QY 542 -----SEKAL-----RKRP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV 578
Db 671 KCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVYVISEKDECIATEV 729

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RESULT 6	
US-10-042-865-107	Sequence 107, Application US/10042865
Publication No. US20040029216A1	
GENERAL INFORMATION:	
APPLICANT: Padigar, Muralidhara	
Li, Li	
APPLICANT: Zerhusen, Bryan D	
Casman, Stacie J	
APPLICANT: Shenoy, Sureah G	
APPLICANT: Spytek, Kimberly	
APPLICANT: Zhong, Mei	
APPLICANT: Gangolli, Esha A	
Burgess, Catherine E	
APPLICANT: Patturajan, Meera	
APPLICANT: Vernet, Corine A.M	
APPLICANT: Taylox, Sarah	
APPLICANT: Tchernev, Velizar T	
APPLICANT: Miller, Charles E	
APPLICANT: Guo, Xiaojia	
APPLICANT: Boldog, Ference L	
Grosse, William M	
APPLICANT: Alsbrook II, John P	
APPLICANT: Gerlach, Valerie L	
APPLICANT: Edinger, Shlomit R	
APPLICANT: Rothenberg, Mark E	
APPLICANT: Ellerman, Karen	
APPLICANT: MacDougall, John	
APPLICANT: Malyankar, Uriel M	
APPLICANT: Millet, Isabelle	
APPLICANT: Peyman, John	
APPLICANT: Smithson, Glenna	
APPLICANT: Gunther, Erik	
APPLICANT: Stone, David	
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of	
Using the Same	
FILE REFERENCE: 21402-537	
CURRENT APPLICATION NUMBER: US/10/042,865	
PRIOR FILING DATE: 2002-05-17	
PRIOR FILING DATE: 2002-01-09	
PRIOR FILING DATE: 2001-01-10	
PRIOR FILING DATE: 2001-02-28	
PRIOR FILING DATE: 2001-03-09	
PRIOR FILING DATE: 2001-04-18	
NUMBER OF SEQ ID NOS: 264	
SOFTWARE: Patent In Ver. 2.1	
SEQ ID NO 107	
LENGTH: 722	
TYPE: PRT	
ORGANISM: Mus musculus	
US-10-042-865-107	
Query Match 72.9%; Score 2466; DB 15; Length 722;	
Best Local Similarity 76.6%; Pred. No. 2.6e-171;	
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;	
Qy 1 MGR-----LLASALLC---VSGVFELKQEFVNKGLL-NRNCRCGS-----GCCTFFR 45	
Db 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKGLLGNRNCRCGSPPACRTFFR 60	
Qy 46 VCLKHYQASVPEPPCTYGSA--TPVLG--SFS-PDGAG-DPAFNSPIRFPFGFTWPGTFS 100	
Db 61 VCLKHYQASVPEPPCTYGSAVTPVLGVDSPFLPDGAGIDPAFNSPIRFPFGFTWPGTFS 120	
Qy 101 LIIIALHTSDPDDL-TENPERLISRL-TQRLH-VGEWSDQLHSSGRTDL-YSYRFVCD 156	
Db 121 LIIIALHTSDPDDLATENPERLISRLTQRLHTVGEWSDQLHSSGRTDLRYSYRFVCD 180	

Qy 157 HYTGEGSVFCRPRDD--FGHFTCG-RGEK-C-PGMKGQYCT-PICLPGC-DQHG-CDKPG 209	
Db 181 HYTGEGSVFCRPRDDAFGHFTCGDRGEKMDPCKMGQYCTDPICLPGCDDQHGVCDEKPG 240	
Qy 210 ECKRVGWQGRYCDCEIRYFCGVHGTQQPWCNQCQEGWGLFCNQDLNVTTHHKPC-NG 268	
Db 241 ECKRVGWQGRYCDCEIRYFCGLHGTQQPWCNQCQEGWGLFCNQDLNVTTHHKPCRN 300	
Qy 269 ATCNTGQSYTCSRPYTG--CE---EBC---PCKNG-SCTDLES--SCTCPPGFYGK 317	
Db 301 ATCNTGQSYTCSRPYTGANCELEVDSCAPSPCKNGASCTDLESFSCTCPPGFYGK 360	
Qy 318 -CELSAMTCADGPCFNGGRC-DNPDDGY-C-CPLG-SGFNCEKD--C-SSPC-NGA-CV 367	
Db 361 VCELSAMTCADGPCFNGGRCSDNPDDGYTCHCPLGSGFNCEKMDLCSGSSPCSNKACV 420	
Qy 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SFC-NGGTC--DVND-SCTCPGY-GKNC-S-P 415	
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGTCRDSVNDFSCTCPGYTKNCAP 480	
Qy 416 VSRCEH-PCNGATCHRR----YCECA-GYGG-NCQFLLPE-PRGP--VD-----BEQ- 458	
Db 481 VSRCEHAPCHNGATCHRGORYMCECAQYGGNQCQFLLPEPPGPMVVDLSEHMSQG 540	
Qy 459 --FPW-AVCAGLV---LILLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503	
Db 541 GPFPMVAVCAGVVLVLLLLGCAA-VVVCVRLKQKHQPPPEPCGGETETMNNLANCQREK 600	
Qy 504 D---SSIGATQIKNTKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540	
Db 601 DVSVTIIGATQIKNTKKADPHDGHGAKKSSFKVRYPTVDYNLVRLDLKDEATVRDTHSK 660	
Qy 541 -----CSBEKAL-----RKRP-SVYSTSKTKYOSVVV--SEKDEC-IAT 576	
Db 661 RDTKQSQSSAGEKIAPTLRGGEIPDRKRPESVYSTKTKYOSVVVLSAEKDECVIAT 720	
Qy 577 EV 578	
Db 721 EV 722	
RESULT 7	
US-10-731-741-4	
Sequence 4, Application US/10731741	
Publication No. US20040171148A1	
GENERAL INFORMATION:	
APPLICANT: Schmitt, Thomas M.	
APPLICANT: Zuniga-Pelucker, Juan-Carlos	
TITLE OF INVENTION: Cell Preparations Comprising Cells of the T Cell	
LINEAGE AND METHODS OF MAKING AND USING THEM	
FILE REFERENCE: 2223-171	
CURRENT APPLICATION NUMBER: US/10/731,741	
CURRENT FILING DATE: 2003-12-10	
PRIOR APPLICATION NUMBER: 60/432,525	
PRIOR FILING DATE: 2002-12-10	
NUMBER OF SEQ ID NOS: 50	
SOFTWARE: Patent in version 3.1	
SEQ ID NO 4	
LENGTH: 722	
TYPE: PRT	
ORGANISM: Mus musculus	
US-10-731-741-4	
Query Match 72.9%; Score 2466; DB 16; Length 722;	
Best Local Similarity 76.6%; Pred. No. 2.6e-171;	
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;	
Qy 1 MGR-----LLASALLC---VSGVFELKQEFVNKGLL-NRNCRCGS-----GCCTFFR 45	
Db 1 MGRSALALAVSALLCQWSSGVFELKQEFVNKGLLGNRNCRCGSPPACRTFFR 60	
Qy 46 VCLKHYQASVPEPPCTYGSA--TPVLG--SFS-PDGAG-DPAFNSPIRFPFGFTWPGTFS 100	
Db 61 VCLKHYQASVPEPPCTYGSAVTPVLGVDSPFLPDGAGIDPAFNSPIRFPFGFTWPGTFS 120	
Qy 101 LIIIALHTSDPDDL-TENPERLISRL-TQRLH-VGEWSDQLHSSGRTDL-YSYRFVCD 156	
Db 121 LIIIALHTSDPDDLATENPERLISRLTQRLHTVGEWSDQLHSSGRTDLRYSYRFVCD 180	

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Db 61 VCLKHQASVSEPPCTCYSAVTPVLGVSFSLPDGAGIDPAESNIRPFPGFTWPGTFS 120
QY 101 LIIEALHTSDPDL--TENPERLISRL--TORHL--VGEWSQDLHSSGRTDL--YSYRPFVCD 156
Db 121 LIIEALHTSDPDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRSYRPFVCD 180
QY 157 HYGEGCSVFCRPRDD--FGHFTCG--RGEK--C--PGWKGOYCT--PICLPGC--DQHG--CDKPG 209
Db 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKRCWDPGWKGOYCTDPICLPGCCDQHGCDKPG 240
QY 210 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQWPQCNQCEGWSGLFCNQDLNYCTHHKPC--NG 268
Db 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQWPQCNQCEGWSGLFCNQDLNYCTHHKPCRG 300
QY 269 ATCTNTGQSGSYTCSCRPGVTG--CE---BEC---PCKNG--SCTDLES--SCTCPPGFYGK 317
Db 301 ATCTNTGQSGSYTCSCRPGVTGANCELEVEDECAPSPCKNGASCTDLEDSFCTCPPGFYGK 360
QY 318 -CELSAMTCADGCFNGGRC--DNPDDGY--C--CPLG--SGFNCEKKD--C--SSPC--NGA--CV 367
Db 361 VCELSAMTCADGCFNGGRCSDNPDDGYTCHCPLGSGFNCEKKMDLCSGSPCSNGAKCV 420
QY 368 DLGNSY--C--COAGF--GR--C--DNVDDCA--SPC--NGGTC--DVND--SCTCPPGY--GKNCS--P 415
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDCCASPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480
QY 416 VSRCEH--PCHNGATCHRR---YCECA--GYGG--NQFLLPE--PPGP--VD-----EQ- 458
Db 481 VSRCEHAPCHNGATCHORQRYMCECAQGYGPNCFLLPEPPGPMVVDLSERHMSOG 540
QY 459 --FPW--AVCAGLV---LLLLGCAA--VVCVRLK--QK-----PE--C--ETETMNNLANCQREK 503
Db 541 GPPFWAVACAGVVLVLLLLGCAA--VVCVRLK--QKQHPPEPCGGTETMNNLANCQREK 600
QY 504 D---SSIGATQIKNTNKK--DFHDK-----KVRYP--VDYNLV--LK-----VHKK 540
Db 601 DVSVSIIIGATQIKNTNKKADFGDHGAKSSPKVRYPTVDYNLVRLDKGDEATVRDTHSK 660
QY 541 -----CSEKAL-----RKRPP--SVYSTKDTKYQSVYV--SEKDEC--IAT 576
Db 661 RDTKQSSAGSEKIAPTLRGGEIPDRKRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720
QY 577 EV 578
Db 721 EV 722

RESULT 8
US-09-908-322-12
; Sequence 12, Application US/0908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-908-322-12

Query Match 72.8%; Score 2462; DB 9; Length 722;
Best Local Similarity 75.9%; Pred. No. 5.2e-171;
Matches 548; Conservative 6; Mismatches 24; Indels 144; Gaps 68;

QY 1 MGR-----LIASALLC---VSGVFELKLOEFVNKKGLL--NRNCCRGG-----GCCTFFR 45
Db 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRCGSGGPPCAGCTFFR 60
QY 46 VCLKHQASVSEPPCTTYGSA--TPVLG--SFS--PDGAG--DPAFSNPIRPFPGFTWPGTFS 100
Db 61 VCLKHQASVSEPPCTTYGSAVTPVLGVSFSLPDGAGIDPAESNIRPFPGFTWPGTFS 120
QY 101 LIIEALHTSDPDL--TENPERLISRL--TORHL--VGEWSQDLHSSGRTDL--YSYRPFVCD 156
Db 121 LIIEALHTSDPDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRSYRPFVCD 180
QY 157 HYGEGCSVFCRPRDD--FGHFTCG--RGEK--C--PGWKGOYCT--PICLPGC--DQHG--CDKPG 209
Db 181 HYGEGCSVFCRPRDDAFGHFTCGDRGKRCWDPGWKGOYCTDPICLPGCCDQHGCDKPG 240
QY 210 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQWPQCNQCEGWSGLFCNQDLNYCTHHKPC--NG 268
Db 241 ECKCRVGMQGRYCDCEIRYPGCVHGTCCQWPQCNQCEGWSGLFCNQDLNYCTHHKPCRG 300
QY 269 ATCTNTGQSGSYTCSCRPGVTG--CE---BEC---PCKNG--SCTDLES--SCTCPPGFYGK 317
Db 301 ATCTNTGQSGSYTCSCRPGVTGANCELEVEDECAPSPCKNGASCTDLEDSFCTCPPGFYGK 360
QY 318 -CELSAMTCADGCFNGGRC--DNPDDGY--C--CPLG--SGFNCEKKD--C--SSPC--NGA--CV 367
Db 361 VCELSAMTCADGCFNGGRCSDNPDDGYTCHCPLGSGFNCEKKMDLCSGSPCSNGAKCV 420
QY 368 DLGNSY--C--COAGF--GR--C--DNVDDCA--SPC--NGGTC--DVND--SCTCPPGY--GKNCS--P 415
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDCCASPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480
QY 416 VSRCEH--PCHNGATCHRR---YCECA--GYGG--NQFLLPE--PPGP--VD-----EQ- 458
Db 481 VSRCEHAPCHNGATCHORQRYMCECAQGYGPNCFLLPEPPGPMVVDLSERHMSOG 540
QY 459 --FPW--AVCAGLV---LLLLGCAA--VVCVRLK--QK-----PE--C--ETETMNNLANCQREK 503
Db 541 GPPFWAVACAGVVLVLLLLGCAA--VVCVRLK--QKQHPPEPCGGTETMNNLANCQREK 600
QY 504 D---SSIGATQIKNTNKK--DFHDK-----KVRYP--VDYNLV-----LK-----UK 536
Db 601 DVSVSIIIGATQIKNTNKKADFGDHGAKSSPKVRYPTVDYNLVRLDKGDEATVRDTHSK 660
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QY 537 VHKCSEKALRR-----PSVYSTSKDTKYQSVVY--SEKDEC-IAT 576
Db 661 RDTKCSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVIAT 720
QY 577 EV 578
Db 721 EV 722

RESULT 9
US-09-783-931-12
; Sequence 12, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Igh-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Isoakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-783-931-12

Query Match 72.8%; Score 2462; DB 10; Length 722;
Best Local Similarity 75.9%; Pred. No. 5.2e-171;
Matches 548; Conservative 6; Mismatches 24; Indels 144; Gaps 68;

QY 1 MGR-----LLASALLC---VSGVFELKLOFVNKKGLL-NRNCRRG-----CCCTFFR 45
Db 1 MGRSALALAVSALLCQWSSGVFELKLOFVNKKGLLNRCNCRGSGPPCACRTFFR 60
QY 46 VCLKHYQASVSPPECTYVGA-TPVLG--SPS-PDGAG-DPAFNPFRFPFGFTWPGTFS 100
Db 61 VCLKHYQASVSPPECTYVGA-TPVLG--SPS-PDGAG-DPAFNPFRFPFGFTWPGTFS 120
QY 101 LIIEALHTSDPDDL-TENPERLISRL-TQRHL-VGEEMSQDLHSSGRDUL-YSYRFVYCDE 156
Db 101 LIIEALHTSDPDDL-TENPERLISRL-TQRHL-VGEEMSQDLHSSGRDUL-YSYRFVYCDE 156

Db 121 LIIEALHTSDPDDL-TENPERLISRL-TQRHL-VGEEMSQDLHSSGRDUL-YSYRFVYCDE 180
QY 157 HYTGEGSVFCRPRDD-FGHFTCG-RGEK-C-PCMKGOYCT-PICLPGC-DOHG-CDKPG 209
Db 181 HYTGEGSVFCRPRDDAFGHFTCGDRGEKMKDPCGWKGOYCTDPICLPGCDDQHGVCYCDKPG 240
QY 210 ECKCRVGMQGRYCDDECIRYPCGVHGTCCQPMQCNQCBGWLFCNQDLNYCTHHKPC-NG 268
Db 241 ECKCRVGMQGRYCDDECIRYPCGVHGTCCQPMQCNQCBGWLFCNQDLNYCTHHKPCNG 300
QY 269 ATCTNTQGSYTCSCRPYTG--CE---BEC---PCXNG-SCTDLES--SCTCPGPFYVK 317
Db 301 ATCTNTQGSYTCSCRPYTGANCELEVBECAPSPCKNGASCTDLESFSCCTCPGPFYVK 360
QY 318 -CELSAMTCADGPGCFNGRC-DNPDGGY-C-CPLG-SGENCEKKD--C-SSPC-NGA-CV 367
Db 361 VCELSAMTCADGPGCFNGRCSDNPDGGYTCPLGSGFNCCKNDLGGSPFCNGAKCV 420
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPGY-GKNCS-P 415
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGTCTCRDSVNDFSCTCPGYTKNCSAP 480
QY 416 VSRCEH-PCNMGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----BEQ- 458
Db 481 VSRCEHAPCHNGATCHRGQRYMCECAQGYGGPCQFLLPEPPGPMVVDLSERHMSQG 540
QY 459 --FPM-AVCAGLV---LLLLGCAA-VVCVRLK-QK-----PE-C--ETETMNNLANCQREK 503
Db 541 GPPFPWAVAGVVLVLLLLGCAA-VVCVRLKQKHQPPPEPCGGGETETMNNLANCQREK 600
QY 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV-----LK 536
Db 601 DVSUSIIGATQIKNTNKKADFHDGHAESKSFKRYPTVDYNLRLKGDDEATVRDTHSK 660
QY 537 VHKCSEKALRR-----PSVYSTSKDTKYQSVVY--SEKDEC-IAT 576
Db 661 RDTKCSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVIAT 720
QY 577 EV 578
Db 721 EV 722

RESULT 10
US-10-417-719-4
; Sequence 4, Application US/10417719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT APPLICATION NUMBER: US/10/417,719
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 08/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-417-719-4

Query Match 72.5%; Score 2454; DB 14; Length 720;
Best Local Similarity 76.4%; Pred. No. 2e-170;
Matches 551; Conservative 6; Mismatches 20; Indels 144; Gaps 71;

APPLICANT: Patturajan, Meera
APPLICANT: Vernet, Corine A.M
APPLICANT: Taylor, Sarah
APPLICANT: Tchernev, Velizar T
APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Boldos, Ference L
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Gerlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Rothenberg, Mark E
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malayankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenna
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: Using the Same
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 108
LENGTH: 714
TYPE: PRF
ORGANISM: Rattus norvegicus

US-10-042-865-108

Query Match 72.0%; Score 2436; DB 15; Length 714;
Best Local Similarity 75.4%; Pred. No. 4e-169;
Matches 538; Conservative 11; Mismatches 29; Indels 136; Gaps 66;

Qy	1	MGR-----LLASALIC---VSGVFELKLOEFVNKKGLL--NRNCCRGG-----GCCTPFR 45
Db	1	MGRSALALAVALLCQWSSGVFELKLOEFVNKKGLLNCRNCGSGGPPCACRTFFR 60
Qy	46	VCLKHQAQSVSPRPCTYGA--TPVLG--SFS-PDGAG-DPAFNPDPFGFTWPGTTF 100
Db	61	VCLKHQAQSVSPRPCTYGSATVAVLVDSFSLPDGAGIDPAFNIRPFPGFTWPGTTF 120
Qy	101	LIIAHLTSDPDDL-TENPERLISRL--TORHL-VGEWSQDLHSSGRTDL-YSYRFVUDE 156
Db	121	LIIAHLTSDPDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLYSYRFVUDE 180
Qy	157	HYEGCVFCPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPQC-DHGG-CDKPG 209
Db	181	HYEGCVFCPRDDAFGHFTCGERGERKMDPGWKGYCTDPICLPGCDDHGCDKPG 240
Qy	210	ECKRVGMQRYCDECIYPGVCHGTQQPWQCNCEGHWGLFCNQDLNYCTHHKPC--NG 268
Db	241	ECKRVGMQRYCDECIYPGCLHGTQQPWQCNCEGHWGLFCNQDLNYCTHHKPCRNG 300
Qy	269	ATCNTNGQSYYTCSCRPYTG--CE---BEC---PKN-GSCTDLES--SCTCPGFYK 317
Db	301	ATCNTNGQSYYTCSCRPYTGANCELEVDCAAPSRCRNGSCTDLEDYSYCTCPGFYK 360
Qy	318	CBSAMTACDGPFCFNGRC--DNPDGGY-C-CPLG-SGFNCBKK---DCSSPC-NGA-CV 367

361 VCBSAMTACDGPFCFNGRCNDPNPDGGYTCHCPAGSGFNCBKKIDLCSPPCSNGAKCV 420

368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GRNCS-P 415

421 DLGNSYLRCQTGFSRYCEDNVDDCASSPCANGGTCDSDVDFSTCTCPGYTRNCSAP 480

416 VSRCEH-PCNHGATCHRR-----YCECA-GYGG-NCOFLPEPPGPV----DBEQPPW-AV 463

481 VSRCEHAPCHNGATCHQGRQRYMCECAQCYGANCOQLPEPPDLLVAOOGSFPMVAV 540

464 CAGLV---LLLIGCAA-VVCVRK-----QKP--EC--ETETNNLANCOREKD---SSIG 508

541 CAGVWLVLILLGCAAAVVCVRKLKQHQPDPDPCGGGETETNNLANCOREKDVSVSIIG 600

509 ATQIKNTNKK-DPH-----DK---KVRYP-VDYNLV-----LKVHKKC---541

601 ATQIKNTNKKADPHGDHGDKSKFKARYPTVDYNLIRDLKGDEATVRDAHSKDTKCSQ 560

542 ---SEKAL-----RKRP-SVYSTSKDTQSVVV--SEKDEC-IATEV 578

661 GSVEBKSTTLRGGEVPDRKRPSVYSTSKDTQSVVLSAEKDECVIATEV 714

RESULT 13

US-09-828-366-21

; Sequence 21, Application US/09828366

; Patent No. US2002010137A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Klein, Robert D.

; APPLICANT: Napier, Mary

; APPLICANT: Wood, William I.

; APPLICANT: Yuan, Jean

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC

; FILE REFERENCE: CELL GROWTH

; CURRENT APPLICATION NUMBER: US/09/828,366

; CURRENT FILING DATE: 2001-04-05

; Prior filing data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 29

; SEQ ID NO 21

; LENGTH: 723

; TYPE: PRF

; ORGANISM: Homo Sapien

US-09-828-366-21

Query Match 71.0%; Score 2401.5; DB 9; Length 723;
Best Local Similarity 75.1%; Pred. No. 1.3e-166;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67

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Db	13	SALLCQWSSGVFELKLOEFVNKKGLLNCRNCGAGPPPCACRTFFRVLCHKYQASVS 72
Qy	57	PEPCTYGA--TPVLG--SFS-PDGAG-DPAFNPDPFGFTWPGTSLIEALTOSP 111
Db	73	PEPCTYGA--TPVLG--SFS-PDGAG-DPAFNPDPFGFTWPGTSLIEALTOSP 132
Qy	112	DOL-TENPERLISRL--TORHL-VGEWSQDLHSSGRTDL-YSYRFVUDEHYEGCVSVC 167
Db	133	DOL-TENPERLISRLATQHLTVGEWSQDLHSSGRTDLKYSYRFVUDEHYEGCVSVC 192
Qy	168	RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPQC-DHGG-CDKPGCKCRVMQGR 220
Db	193	RPRDDAFGHFTCGERGERKVCNPGWKPYCTEPICLPGCDEHQGFCDKPGCKCRVMQGR 252
Qy	221	YDECIYRPGCVHGTQQPWQCNCEGHWGLFCNQDLNYCTHHKPC--NGATCTNTGOSY 279
Db	253	YDECIYRPGCLHGTQQPWQCNCEGHWGLFCNQDLNYCTHHKPCNGATCTNTGOSY 312

Search completed: November 29, 2004, 13:42:04
Job time : 62.226 secs

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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match          71.0%; Score 2401.5; DB 14; Length 723;
Best Local Similarity 75.1%; Pred. No. 1.3e-166;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

Qy      7  SALLC---VSGVFELKQBFVNKKGLL-NRNCRRG-----GCCTFFRVCLKHQASVS 56
Db      13  SALLCQVSSGVFELKQBFVNKKGLLGNRNCRRGAGPPCACRTFFRVCLKHQASVS 72

Qy      57  PPPCTYGS-A-TPVLG--SFS-PDGAG-DPAFSNPIRPFPGFTWPTGTFSLIIIEALHTDSP 111
Db      73  PPPCTYGS-A-TPVLGVSFSLPDGGGADSAFSPNPIRPFPGFTWPTGTFSLIIIEALHTDSP 132

Qy      112  DDL-TENPERLLSRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDDEHYHGECSVFC 167
Db      133  DDLATENPERLLSRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDDEHYHGECSVFC 192

Qy      168  RPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGCD-QHG-CDKPGCEKCRVGMQGR 220
Db      193  RPRDDAFGHFTTGERGEKVCNFGWKGPYCTEFICLPGCDDEQHGFCDXPGCEKCRVGMQGR 252

Qy      221  YCDECIRYPCGVHGTQQPWCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279
Db      253  YCDECIRYPCGLHGTQQPWCNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY 312

Qy      280  TCSCRPGYTG--CE---EBC---PCKN-CSCTDLES--SCTCPPGPGYK-CELSAMTCAD 327
Db      313  TCSCRPGYTGATCELGIDECPSCKNGSGCTDLENSYSCCTCPPGPGYKICELSAMTCAD 372

Qy      328  GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376
Db      373  GPCFNGGRCSDSPDGGYSCPCPVYSGFNCEKKIDYCSSSPCSNGAKCVDLDGAYLCRCQ 432

Qy      377  AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425
Db      433  AGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSAPVSRCEHAPCHN 492

Qy      426  GATCHRR-----YCECA-GYGG-NCQPLLPE-PPGP--VD-----EEQ-----EPW-AVCAGL 467
Db      493  GATCHERHRYVCECARGYGGPNCQPLLPEPPGPAVDLTBKLEGGGPPFPWAVACAGV 552

Qy      468  VL---LLLGCAA-VVCVRL--KQKPEC-----ETETMNLANCOREKD---SSIGATQI 512
Db      553  ILVLLMLLGCAAVVVCVRLRLOKRPDPADPCRGETETMNLANCOREKDISVSIIGATQI 612

Qy      513  KNTNKK-DPH-----DK---KVRYP--VDYNLV-----LKVHKEC-----S 542
Db      613  KNTNKADPHGDSADKNGFKARYPAVDYNLVQDLKGGDDTAVRDAHSKEDTKCQPGSSG 672

Qy      543  EEKAL-----RKRP-SVYSTSKTKYQSVYV---SEKDEC-IATEV 578
Db      673  EEKGTPTTLRGGEASERKRPDSGCSKTKYQSVYVVISEEKDECVIATEV 723
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:16:29 ; Search time 14.4855 Seconds
(without alignments)
3839.238 Million cell updates/sec

Title: US-09-783-931-13
Perfect score: 3383
Sequence: 1 MGRLLASALLCVSGVFELK.....DTKYQSVVYSEKDECIATEV 578

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2489	73.6	728	2 I50719	C-Delta-1 - chicke
2	2466	72.9	722	2 I48324	DELTA-like 1 - mou
3	1329.5	39.3	685	2 JC7570	Delta-4 protein -
4	1288.5	38.4	686	2 JC7569	Delta-4 protein -
5	1086.5	32.1	833	2 S19087	gene Delta protein
6	1085.5	32.1	832	2 A31246	neurogenic protein
7	1084.5	32.1	880	2 S00670	neurogenic repetit
8	935.5	27.7	1220	2 A56136	jagged protein pre
9	758.5	22.4	1408	2 S16148	gene serrate prote
10	496.5	14.7	2437	2 S42612	transmembrane prot
11	492.5	14.6	2524	2 A35844	Xotch protein - Af
12	491	14.5	385	2 S53718	homeotic protein d
13	489.5	14.5	2531	2 A46019	notch-1 protein -
14	485	14.3	1203	2 A49175	Notch B protein -
15	484.5	14.3	2531	2 S18188	notch protein homo
16	484	14.3	385	2 A54785	preadipocyte facto
17	478	14.1	2471	2 A49128	cell-fate determin
18	473.5	14.0	2531	2 T31070	notch homolog - se
19	464	13.7	2318	2 S43306	notch 3 protein -
20	461	13.6	383	2 S53716	delta-like homeoti
21	459	13.6	2555	2 A40043	notch protein homo
22	456.5	13.5	2352	2 T30201	Notch homolog prot
23	454	13.4	1064	2 A40136	fibropellin Ia - s
24	450	13.3	308	2 JC7125	epidermal growth f
25	448	13.2	2703	1 A24420	notch protein - fr
26	445.5	13.2	2321	2 S78549	notch3 protein - h
27	441	13.0	2139	2 A35672	crumbs protein - f
28	434	12.8	1964	2 T09059	notch4 - mouse
29	424.5	12.5	861	2 A48825	Notch homolog Motc

30	421.5	12.5	1295	2 A32901	glpi protein precu
31	413.5	12.2	1429	2 S06434	homeotic protein 1
32	405	12.0	1620	2 T27283	hypothetical prote
33	400	11.8	1722	2 E89753	protein FlilC7.4 [i
34	397.5	11.7	1574	2 T13954	MEGF6 protein - ra
35	387	11.4	473	2 A56175	adhesive plaque pr
36	386.5	11.4	2201	2 A32160	tenascin-C - human
37	378	11.2	570	2 A48836	fibropellin C prec
38	376.5	11.1	2019	1 J01322	tenascin precursor
39	375	11.1	1372	2 T59333	hypothetical prote
40	371	11.0	1746	1 S19694	tenascin precursor
41	367	10.8	3566	1 A40701	tenascin-X precurs
42	367	10.8	4006	2 T09070	probable tenascin
43	365	10.8	1111	2 T26972	hypothetical prote
44	352.5	10.4	1810	1 A32230	tenascin precursor
45	350	10.3	4135	2 T42629	tenascin-X - bovin

ALIGNMENTS

RESULT 1

150719
C-Delta-1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50719
R:Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A:Title: Expression of a Delta homologue in prospective neurons in the chick.
A:Reference number: I50719; MUID:95319507; PMID:7596411
A:Accession: I50719
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <H>
A:Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:9882411; PIDN:AAC59689.1; PID:98824
C:Superfamily: delta-4 protein; EGF homology
F:299-332/Domain: EGF homology <EGX1>
F:339-370/Domain: EGF homology <EGF1>
F:416-447/Domain: EGF homology <EGX2>
F:454-485/Domain: EGF homology <EGF>
F:492-523/Domain: EGF homology <EGF3>

Query Match 73.6%; Score 2489; DB 2; Length 728;

Best Local Similarity 76.0%; Pred. No. 1.1e-145; Mismatches 9; Indels 144; Gaps 65;

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Qy	49	KHYQASVSPBPCTYGSATPVILG--SFS-PDGAG--DPAFSNPIRPFPGTWTGTSLLI	102
Db	71	KHYQASVSPBPCTYGSATPVILGANSFSPDGAGGADPAPSNPIRPFPGTWTGTSLLI	130
Qy	103	IEALHTDSPDL-TENPERLISRL-TORHL-VGSEWSQDLHSSGRTDL-VSYRFVCDHY	158
Db	131	IEALHTDSPDLTTENPERLISRLATQRLAVGEWSQDLHSSGRTDLKYSYRFVCDHY	190
Qy	159	YGECSVFCPRPD--FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC	211
Db	191	YGECSVFCPRPD--FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC	250
Qy	212	KCRVWGQRYCDICIRYPCVCHGTCCQPMQCNCOEGHGLFCNQDLNCTHHKPC-NGAT	270
Db	251	KCRVWGQRYCDICIRYPCVCHGTCCQPMQCNCOEGHGLFCNQDLNCTHHKPC-NGAT	310
Qy	271	CTNTGQSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLSES--SCTCPGFGYK-C	318
Db	311	CTNTGQSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLSES--SCTCPGFGYK-C	370
Qy	319	ELSAWTCADGFCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL	369

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Db 371 ELSAMTCADGCFNGRCRDTNDGGYSRCPLGYSGFNCEKKIDYCSSSPCANGACQVDL 430
QY 370 GNSY-C-CQAGF-GR-C-DNVDDCA-PC-NGTCD--VND-SCTCPPGY-GKNCS-PVS 417
Db 431 GNSYICQCAGTGRHCDNDVDCASFPCVNGGTQCDGVNDYSCTCPPGYGKNCSTPVS 490
QY 418 RCEH-PCNHGATCHRR----YCECA-GYGG-NCQFLLPEPP-GPV------DEQ 458
Db 491 RCEHNPCHNGATCHEHSNRYVCECARGYGLNCQFLLPEPPQGPVIVDTFKYTGQNSQ 550
QY 459 FFW-AVCAGLVL----LLLGCAA-VVCRVLK----QKPEC----ETETMNNLANCQREKD- 504
Db 551 FFWIACAGIILVLMLLGCAIVVCRVLKVQKRHHQPEACRSEETMNNLANCQREKDI 610
QY 505 --SSIGATQIKNTNKK-DPH----DK----KVRYP-VDYNLVK------HKC- 541
Db 611 SISVIGATQIKNTNKKVDFHSDNSDNGYKVRYPSVDYNLVHELKNEDEVKEHGKCEAK 670
QY 542 -----SEKAL-----RKEP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
Db 671 CBTYDSEBEKSAVLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEKDECIATEV 728

RESULT 2
I48324
DELTA-like 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48324
R:Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A:Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin
A:Reference number: I48324; PMID:95401858; PMID:7671806
A:Accession: I48324
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-722 <RES>
A:CROSS-references: UNIPROT:Q61483; EMBL:X80903; NID:9806569; PIDN:CAAS6865.1; PID:9806569
C:Genetics:
A:Gene: Dll1
C:Superfamily: delta-4 protein; EGF homology
F:331-362/Domain: EGF homology <EGF2>
F:446-477/Domain: EGF homology <EGF>
F:484-515/Domain: EGF homology <EGF1>

Query Match 72.9%; Score 2466; DB 2; Length 722;
Best Local Similarity 76.6%; Pred. No. 2.7e-144;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY 1 MGR-----LLASALIC---VSGVFELKLOEFVNKKGLL--NRNCCRGG-----GCTTFR 45
Db 1 MGRSALALAVVSALLCQWSSGVFELKLOEFVNKKGLGNRNCRCGGSGGPPCACTTFR 60
QY 46 VCLKHYQASVPEPPTCYGSA--TPVLG--SFS-PDGAG-DPAFNSPIRPFPGTWPGTFS 100
Db 61 VCLKHYQASVPEPPTCYGSAVTPVLGVDSFSLPDGAGIDPAFNSPIRPFPGTWPGTFS 120
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL--YSYRPFVCD 156
Db 121 LIIEALHTDSPDDLATENPERLISRLTQRHLTVGEWSQDLHSSGRTDLRYSYRPFVCD 180
QY 157 HYYGECVSFCRPRDD-FGHFTCG-RGEK-C-PGWKGYCT-PICLPCC-DQHG-CDKPG 209
Db 181 HYYGECVSFCRPRDDAFGHTCGDGEKXDPGWKGYCTDPICLPGCCDQHGCDKPG 240
QY 210 ECKRCRVGMOGRYDCEIRYPGCVHGTQCPQWQNCQEGWGLFCNQDLNYCTHHKPC-NG 268
Db 241 ECKRCRVGMOGRYDCEIRYPGCVHGTQCPQWQNCQEGWGLFCNQDLNYCTHHKPCRG 300
QY 269 ATCTNTGQSYTSCSRPGYTG--CE-----BEC---PCKNG-SCTDLBS--SCTCPGFGYK 317
Db 301 ATCTNTGQSYTSCSRPGYTGANCELEVEDCAPSPCKNGASCTDLBDSFCTCPPFGYK 360
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QY 318 -CELSAMTCADGCFNGRC--DNDPGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367
Db 361 VCELSAMTCADGCFNGRCSDNDPGGTCHCPLGFSGFNCEKKMDLCOSSPSCNGAKCV 420
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCDSDVNDFSCTCPGTYGKNCSAP 480
QY 416 VSRCEH-PCNHGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458
Db 481 VSRCEHAPCHNGATCHQRQRYMCECAQGYGPNCOFLLPEPPGPMVVDLSERHMESOG 540
QY 459 --FPW-AVCAGLV----LLLGCAA-VVCRVLK-QK----PE-C--ETETMNNLANCQREK 503
Db 541 GPPFWAVACAGVVLVLLLGCAAVVCRVLKQKHQPPPEPCGGTETMNNLANCQREK 600
QY 504 D---SSIGATQIKNTNKK-DPHDK-----KVRYP-VDYNLV--LK-----VHKK 540
Db 601 DVSVSIIIGATQIKNTNKKADPHGDHGAKKSPKRYPTVDYNLVRLDKGEATVRDTHSK 660
QY 541 -----CSEKAL-----RKEP-SVYSTSKDTKYQSVYV--SEKDEC-IAT 576
Db 661 RDTKCQSOSAGEEKIAPTLRGGEIPDRKRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720

QY 577 EV 578
Db 721 EV 722

RESULT 3
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C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7570
R:Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A:Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A:Reference number: JC7569; PMID:21064937; PMID:11134954
A:Accession: JC7570
A:Molecule type: mRNA
A:Residues: 1-685 <YON>
A:CROSS-references: UNIPROT:Q9NR61; DBJ:AB043894
C:Comment: This protein, a member of the Notch family of proteins, is a transmembrane re-
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C:Genetics:
A:Gene: delta-4
C:Superfamily: delta-4 protein; EGF homology
C:Keywords: transmembrane protein

Query Match 39.3%; Score 1329.5; DB 2; Length 685;
Best Local Similarity 46.4%; Pred. No. 1.6e-74;
Matches 314; Conservative 81; Mismatches 154; Indels 127; Gaps 52;

QY 13 SGVFLKLOEFVNKKGLL--NRNCCRGCGCCTFFRVCLKHQYASVPEPPTYGS--ATPV 69
Db 27 SGVFLQLOEFNINERGVLASRPGC--EPGCTFFRVCLKHQYAVVSP-CPCTFTGTSTPV 83
QY 70 LG--SFSPDGADPAFNSPIRPFPGTWPGTFTSLIIEALHTDSPDDLTEN---PERLISR 124
Db 84 LGTNSFAVRDDSSGGGRNPQLPFPNFTWPGTFTSLIIEAWHAPG-DDLRPEALPPDALISK 142
QY 125 LT-QRHL-VGEWSQDLHSSGRTDL--YSYRPFVCDHEHYGEGSVFCRPRDD-FGHFTC-- 178
Db 143 IAIQSLAVGQWMLDEQTLTLRLRYSYRVICSNYYGDNCSRLCKKNDHFGHYVCP 202
QY 179 -GRGCKCPGWKGYC-TPICLPCC-DQHG-CDKPECKRCRVGMOGRYDCEIRYPGCVHGT 234
Db 203 DGNLSCLPFWTGEYCOQPICLSGCHEQNGYCSKPAECLCPGWQGLNCECLPHNGCRHG 262
QY 235 TCQQPWCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQSYTSCSRPGYTG--CE 291
Db 263 TCSTPWQCTCDGWSGLFCDQDLNYCTHHS PCKNGATCSNGQSYTCTCRPGYTGVDCE 322
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Qy	290	-CE---BEC---PCKN-GSCTDLESS--CTCPGPFYGK-CELSAMTCADGCPFNHGRC--	330
Db	321	HCELGSLKSCASNPCRNGGCKQDQENSVHCLCPPGYVGHCEHSTLTLCADSPCFNGGSCRE	380
Qy	337	DNPDDGYCC---PLGSGFNCCK--DC-SSPC--NGACVDLGNYSYCCQA--GF--GRCD--	383
Db	381	RNQGSSYACECPNFTGTSNCEKKVDRCTNPNPCANGGQCONRPSRTCRCRPGFTGTHCEL	440
Qy	384	NVDDCA-SPC-NGGTC-DVND--CTCPBGY-GKNGSPVSRCEH-----PCHNGATCH--	430
Db	441	HISDCARSCAAGGTCHDLENGPVCTCPAGFSGRCE--VRITHDACASGCFNGATCYT	498
Qy	431	-----RRYCECA-GY-GGNCQFLPPLPPGPFVDEEQPW-AVCAG-----LVLLLLGCAA	476
Db	499	GLSPNNFVNCNCPYGFVGRCEFPVGLPP-----SPPWVAVSUGVLWLLVLLVMVVA	552
Qy	477	VVCVRLKQPEKETETWNLNLCQREKDSIGATQIKNTN-KKDPH-----DKKV	525
Db	553	VQRLRLRRPDDRESAMNLSDFQ--KDNLPAAQLKNTNQKKELEVDGCLDKSNCGKLG	610
Qy	526	RYPVDNLV-----LVHKKCSSEKALRKRPVSVYTSKDT	560
Db	611	NHTLDNLNAPLLGRCGMGPKYPHSDKSLGEKVPLRLHSEKPE-----CRISAICSPRDS	665
Qy	561	KYQSVYV--SEKDEC-IATEV	578
Db	666	MYQSVCLISEERNECVIATEV	686

RESULT 5
 S19087
 gene Delta protein precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S19087
 R:Muskavitch, M.A.T.
 A:Reference number: S19087
 A:Accession: S19087
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-833 <MUS>
 A:Cross-references: UNIPROT:P10041; EMBL:Y00222
 C:Genetics:
 A:Gene: FlyBase:D1
 A:Cross-references: FlyBase:FBgn0000463
 C:Superfamily: neurogenic protein delta; EGF homology
 F:335-371/Domain: EGF homology <EGF1>
 F:378-415/Domain: EGF homology <EGX1>
 F:457-488/Domain: EGF homology <EGF>
 F:533-564/Domain: EGF homology <EGF3>

Query Match	32.11%	Score	1086.5	DB 2	Length	833			
Best Local Similarity	38.11%	Pred. No.	1.6e-59						
Matches	252	Conservative	67	Mismatches	177	Indels	165	Gaps	40

Qy	3	RLLASALLCV-----SCVFELKLOEFVNNKGLLNR-NCCRG-----GGCTTF	43
Db	5	KCLLTAFICFTVIVQHSSGSFELRLKYFSNPHGRDNEGRCCSGESDGTGKCLGSCKTR	64
Qy	44	FRVCLKHYQASVPEPPCTYGSA-TPVLGSFSPDGAG-----DPAFSNIRPFPFGFTWPG	97
Db	65	FRVCLKHYQATDITTSQCTYGDVITFILGENSVNLTDQRFQNKGFNTFIQPPFSFWPG	124
Qy	98	TFSLIIELHTDSDDLTPENPERLISRLTORHL--VGEEMSOQLHSSGRDIL--YSYRFVC	154
Db	125	TFSLIVEAWHDTNNSGNARTNKLILQRLLVQVLEVSSEWTKNKSESQVTSLEYDPRVTC	184
Qy	155	DEHYVGECSVFCRRPDD--FGHTGCR-GE--KCFGWKQYIC-TPICLPGCQHQGCDKPG	209
Db	185	DLNLYTSGCAKCFRRDSDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCBHGHCDFEN	244


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Qy 5 LASALLCV-----SGVFELKLOEFVNKKGLLNR--NCCRG-----GQCCTFR 45
Db 7 LITAFICTVIVQVHSSGSEFELRLKYFSNDRGRDNEGRCCSGESDAGTKGLGSKCTRFR 66
Qy 46 VCLKHQYQASVPEPCTYGS--TPVLGFSFDGAG-----DPASNPIRPFPGTWGTF 99
Db 67 LCLKHQYQATIDTTSOCTYGVDTPILGNSVNLTAQRFQNKGFNPQFPFSFWGTF 126
Qy 100 SLIIIEALHTDSPDLTENPERLISRLTORHL--VGEWSQDLHSSGRTDL--YSYRFVCD 156
Db 127 SLIVEAHDWTNNSGARTNKLIIQRLVQVLEVSSEWTKNSBSQYTSLEYDRVITCDL 186
Qy 157 HYYGEGSVFCRPRDD--FGHTTCGR--GE--KCPGWKGYC--TPICLPGCDQHQGDKPGE 211
Db 187 NYYGSGAKFCRPRDDSGFHSCTSETGIIILCTGWQGDYCHIPKCAKGECHGDKPNQC 246
Qy 212 KCRVGMGRYDCICIRYPCGVHGTCTQCPWQCNCOEGWGLFCNODLNYCTHHKPC--NGAT 270
Db 247 VCQLGWKALCNCEVLEPNCIHGTCNKPWTICNEGWGLYCNQDLNYCTNHRPCXNGGT 306
Qy 271 CTNTGQGSYTCSCRPGYTG--CEBE-----SCTCPPGYG--KCELSAMTCADGP 299
Db 307 CFNTGEGLYTCKCAPGYSGDDCENIYSCDADVNPQNGGTCIDSPHTKTKYKCHRWG 366
Qy 300 -----SCTD-----LES-----SCTCPPGYG--KCELSAMTCADGP 329
Db 367 SGKMCBEKVLTCSDKPKHQICRNVRPGLGSKGQGYQCEPIGYSGPNCDLQDNCSPNP 426
Qy 330 CFNGGRCDNPGGYCCPLG--SGFNCEK--DC--SSPC--NGACVDLGNISYCCOA--GF-- 379
Db 427 CINGGSC--QPSGKCTCPSGFSGTCTNIDCLGHQCENGGTCIDMVNQYRCQCVPGFHG 485
Qy 380 GRCDN--VDDC--ASPC--NGGTC--DVND--SCTCPPGY--GKNS--PVSCEH--PCHNGAT 430
Db 486 THCSKVDLCLIRFCANGGTCNLNDYQCTCRAGFTGKDCSVIDECSSGFCXNGGTCM 545
Qy 431 RRY-----CECA--GYGNCQFLPPEPPGVDBEQPP-----QCBESYDSTFDAQH 460
Db 546 NRNVNSFECVCAQFRGK-----QCBESYDSTFDAQHGYATTQARADGLANAQV 595
Qy 461 -----WAVCAGLVLLGCAAVVCLRKORPECETETMNNLANCQREKDSIGATQKN 514
Db 596 VLIIVFVAMPVLAVIAAC--VVFCKRKRRAQEKDN-----AEARKQNEQNAVATMHN 649

RESULT 8
A56136
jagged protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
C;Accession: A56136
R;Lindeell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
Cell 80, 909-917, 1995
A;Title: Jagged: a mammalian ligand that activates Notch1.
A;Reference number: A56136; MUID:95211842; PMID:7697721
A;Accession: A56136
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1220 <LIN>
A;Cross-references: GB:L38483
F;379-410/Domain: EGF homology <EGF1>
F;492-523/Domain: EGF homology <EGF>
F;634-665/Domain: EGF homology <EGF2>

Query Match 27.7%; Score 935.5; DB 2; Length 1220;
Best Local Similarity 38.4%; Pred. No. 4.1e-50;
Matches 213; Conservative 64; Mismatches 159; Indels 119; Gaps 37;

Qy 5 LASALLC-----VSQVFELKLOEFVNKKG--LLNRNCRGGG-----CCTF 43
Db 16 LLLALLCALRAKVCAGSQGFELLSQNVNGLQNGCCNEPTLVRPYKTRDECDTY 75
Qy 44 FRVCLKHQYQASVPEPCTYGS--ATPVLG-----SFSFDGAGDPAFNSPIRPFPGTWPGT 98
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Db 76 FKVCLKEYQSRVTAGGPCSGSGSTPVIGGNTFNLKASRGND---RNRIVLPFFFAWPRS 132
Qy 99 FSLIIIEALHTDSPDLTENPERLISRLTORHLV--GEWSQDLHSSGRTDL--YSYRFVCD 155
Db 133 YTLIVEA--WDSSND--TIQDPSIIIEKASHSGMINPNSQWQTLKONTGLAHPEYQIRVTCD 189
Qy 156 EHYGEGSVFCRPRDD--FGHTTCGR--GEK--CPGWKGYC--PICLPFGCD--QHG--CDKP 208
Db 190 DHYYGFCNKFRCRPRDD--FGHYACDQNGKNTCMEGMWGPCNKAICRQCSKPHGSKLP 249
Qy 209 GECKRVGMGRYDCICIRYPCGVHGTCTQCPWQCNCOEGWGLFCNODLNYCTHHKPC--N 267
Db 250 GDRCQYQWGLYCDKCIPIHPCGVHGTCTNBPWQCLCTNMGQQLCDKDLNYCYGTHQPCLN 309
Qy 268 GATCTNTGQGSYTCSCRPGYTG-----CEE-----ECPCK----- 297
Db 310 RTGCSNTGPKYQCSCEPESGPNCEIAEACIACISDPCNHRGSKCETSSGFECECSPGWTG 369
Qy 298 -----NGSCTDLIES--SCTCPPGYGK--CELSAMTCADGPCFNGGRCD 337
Db 370 PTCSTNIDDCSPNNSHGGTCQDLVNGFKVCVPPQWTGKTQLDANECEAKPCVNARSCK 429
Qy 338 NPGGY---CCPLGSGNCS--KDCSSPC--NGACVDLGNISY--CCQAGFG--RCD--NV 385
Db 430 NLIASYVCDCLPGMWGQNCININDCLGQCQNDASCRDLVNGYRCICPPGYAGDHCDERDI 489
Qy 386 DDCAS--PC--NGGTC--DVND--SCTCPPGYGK--CS--PVSCE--HPCHNGATCHRR---Y 433
Db 490 DECANPCLNGHGCQNEINRFQCLPTGFGSLNQLDIDYCEPNPCQNGAQCYNRASDYF 549
Qy 434 CECAG--YGGNCQFL 446
Db 550 CKCPEDYEGKNCSHL 564

RESULT 9
S16148
gene serrate protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16148; S16878; A36666
R;Thomas, U.; Speicher, S.A.; Knaust, E.
Development 111, 749-761, 1991
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a co-
A;Reference number: S16148; MUID:91347903; PMID:1840519
A;Accession: S16148
A;Molecule type: mRNA
A;Residues: 1-1408 <THO1>
A;Cross-references: UNIPROT:P18168; EMBL:X56811
R;Thomas, U.
submitted to the EMBL Data Library, November 1990
A;Reference number: S16878
A;Accession: S16878
A;Molecule type: mRNA
A;Residues: 1-1351,'T',1353-1408 <THO2>
A;Cross-references: EMBL:X56811; NID:98563; PID:98564
R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential fo
A;Reference number: A36666; MUID:91099666; PMID:2125287
A;Accession: A36666
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15,20-26,'A',28-1408 <FLE>
A;Cross-references: GB:M35759; NID:9158605; PID:9158606
C;Genetics:
A;Gene: FlyBase:Ser
A;Cross-references: FlyBase:FBgn0004197
C;Keywords: glycoprotein; transmembrane protein
F;1-84/Domain: signal sequence #status predicted <SIG>
F;85-1408/Product: gene serrate protein #status predicted <MAT>
F;85-1221/Domain: extracellular #status predicted <EXT>
```


Db 792 E-----CASNPCL-----NOGSCIDDVAGFKCNC 815

RESULT 11

A35844

Xotch protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004

C:Accession: A35844

R:Coffman, C.; Harris, W.; Kintner, C.

Science 249, 1438-1441, 1990

A:Title: Xotch, the Xenopus homolog of Drosophila notch.

A:Reference number: A35844; MUID:90385285; PMID:2402639

A:Accession: A35844

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-2524 <COF>

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C:Keywords: transmembrane protein

F:146-177/Domain: EGF homology <EGX1>

F:184-215/Domain: EGF homology <EGX1>

F:222-254/Domain: EGF homology <EGF>

F:456-487/Domain: EGF homology <EGX2>

F:757-788/Domain: EGF homology <EGF3>

F:1025-1056/Domain: EGF homology <EGX3>

F:1924-1956/Domain: ankyrin repeat homology <AN1>

F:1957-1989/Domain: ankyrin repeat homology <AN2>

F:1991-2023/Domain: ankyrin repeat homology <AN3>

F:2024-2056/Domain: ankyrin repeat homology <AN4>

F:2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 14.6%; Score 492.5; DB 2; Length 2524;

Best Local Similarity 28.4%; Pred. No. 1.2e-22;

Matches 182; Conservative 61; Mismatches 190; Indels 208; Gaps 47;

Qy 10 LCVSGVFELKQEFVKNKGLLRNCCRGCGC-----CTFRVCLKHQYQASVSEPEP 59

Db 322 VCVNGWTGEDCSE--NIDDCANAAHSGATGCHDRVASFYCYCPHGRGTGLLCHLDNACISN 379

Qy 60 PCTVGS---ATPVLGS---FSPDGAGDPAFSNRFPFPFTWPTGFTSLIETHLTDSPDD 113

Db 380 PCNENSGNDTPNVNGKAICTCPPTGTPACNDV-----DECS 417

Qy 114 LTPENPERLISRLTORHLVGEWSQDLHSSGRDLYSRFVCDHYEGGCSV-----FCR 168

Db 418 LGANPCRGGRCT-----NTLGSFQCNCPOGYAGPRCIDVNECLSN 459

Qy 169 P-----RDPFGHFTCGRGK-C-PGMKGOYC-TPI-----CLPGCDQHGCD 206

Db 460 PCQNDSTCLDQIGBFQC---ICMPGYEGLYCETNIDECASNPLHNGKCIDKINEFRCD 515

Qy 207 KPG-----EKCVRVGWGRVCD-----ECIRYPG 230

Db 516 CPTGFSNLCQHDDECTSTPCKNKAKCLDGPNSYTCQCTEGFGRHCEQDINFCIDP- 574

Qy 231 CVHGTCTCOO---PMQCNQCGWGLFCNODLNYCTHHKPC-NGATCTNTGQSYTCSCRPG 286

Db 575 CHYGTCKDGTATFTCLCRPGYTGRLCDNDINECL-SRPCLNGGQCTDRENG-YICTPKG 632

Qy 287 YTG---CE---BECP---CKNGSCDTLES--SCTCPPPGFYGK-CBLSAMTCAAGPCFNGGR 335

Db 633 TTGVNCEKTKIDDCASNLCDNGKCIDKIDGVECTCEPGYTGKLCNININECDNSNCRNGGT 692

Qy 336 CDNPDGGYCCPLSGGFN-----CEKDC-SSPC-NGACVDLGNYS-C-CQAGP--GRCD- 383

Db 693 CKDQINGFTVCPPGYHDHMCCLSEVNECNPNPCIHGACHGVNGYKDCBAGSGSNCDI 752

Qy 384 NVDDCAS-PC-NGCTC-DVNDN--CTCPPGY-GKNC-SPVSR-C-EHPCNGATCHRRYCE 435

Db 753 NNNECESNPNNGGTCXDMTGAYICTKAGFSGNCQTNINECSNPNCLNHGTC---IDD 809

Qy 436 CAGYGGNCQFLLPEPPGFVDEQPPWAVCAGLVLLLLGCAAVVCV---RLKQPECECTET 492

Db 810 VAGYKNC--MLP-----YTGAICEA--VLAPCAGSPCKNGGRCKESEDFTFTS 854

Qy 493 -----MNNLAN--COREKDSIGGATQIKNTN 516

Db 855 CECPPGQGGTCEIDMNECVNRRPCRN-----GAT-CONTN 888

RESULT 12

S53718

homoeotic protein dlx - mouse

C:Species: Mus musculus (house mouse)

C>Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S53718

R:Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.

Biochim. Biophys. Acta 1261, 223-232, 1995

A:Title: dlx, pG2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like sup

A:Reference number: S53716; MUID:95226449; PMID:7711066

A:Molecule type: mRNA

A:Accession: S53718

A:Residues: 1-385 <LEE>

A:Cross-references: UNIPROT:Q09163; EMBL:U15980; NID:G562107; PIDN:AAB60495.1; PID:G5621

C:Superfamily: preadipocyte factor 1; EGF homology

C:Keywords: transmembrane protein

F:54-85/Domain: EGF homology <EGF1>

F:92-124/Domain: EGF homology <EGF>

F:131-167/Domain: EGF homology <EGF3>

F:214-246/Domain: EGF homology <EGX1>

F:303-332/Domain: transmembrane #status predicted <TM1>

Query Match 14.5%; Score 491; DB 2; Length 385;

Best Local Similarity 32.8%; Pred. No. 3.2e-23;

Matches 126; Conservative 39; Mismatches 95; Indels 124; Gaps 23;

Qy 173 FGHTFCRGKCKPGWKQGYCTPCLPCD-QHG-CDKPGCKCRVGHQGYCDECIYPG 230

Db 17 FGHSTYGAE-----CDPPCDPQYGFCEADNVCRCHVGEPLCDCKCVTAPG 62

Qy 231 CVHGTCTCOOPQCNQCGWGLFCNODLNYCTHHKPCNGATCTNTGQSGYTCSCRPGVTG- 289

Db 63 CVNGVKCEPQCIKQGWGDKFCFIDVRACTSTPCANNCTCVLEKQYECSTTPGSGK 122

Qy 290 -CBEEC-----PCKN-GSCTDLE-----SSTCTPPGYGK-CELSAMT--CADGPCF 331

Db 123 DCQHKAGPCVINGSPCHGACVDDQASHASCLCPGPGFSGNFCFVAATNSCTPNPCE 182

Qy 332 NGRCDNPDGCGYCPGLSGFNCCKKDCSSPCNGACVDLGNYSQCGAGFGRCDNVDDCAS- 390

Db 183 NDGVCTDIGDFRCRCPAGE--VDKTCRP-----VSNCSAG 217

Qy 391 PC-NGGTC---DVNDSTC-PGYGKNC-----SPVSRCEHPCHNGATCHRRYCECAG 438

Db 218 PCQNGGTCLQHTQVSFELCKPFPMPGTCAKRGASPVQVTHLP-----SG 263

Qy 439 YGNCQFLLPEPPG---PVDE-EQF-----PWAVCAGLV-----LL 470

Db 264 YGLTYRL---TFGVHELVPQPEQHLKVSVMKELNKSFTLLTEGQAICFTILGLVLSLV 319

Qy 471 LLGCAAVVCLKQKPECECTETWN 494

Db 320 VLGTVAIVFLN-----KCTWVSN 338

RESULT 13

A46019

notch-1 protein - mouse

N:Alternate names: notch protein

C:Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C:Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109

R:Gel Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid

Genomics 15, 259-264, 1993

A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
 F:143-174/Domain: EGF homology <EGX1>
 F:482-513/Domain: EGF homology <EGF1>
 F:560-591/Domain: EGF homology <EGF>
 F:674-705/Domain: EGF homology <EGF2>
 F:712-743/Domain: EGF homology <EGF3>
 F:836-867/Domain: EGF homology <EGX3>

```

Query Match      14.3%; Score 485; DB 2; Length 1203;
Best Local Similarity 25.2%; Pred. No. 1.9e-22;
Matches 184; Conservative 59; Mismatches 178; Indels 310; Gaps 48;

Qy 34 CRRGGCCCTFRVCLKHQYQASVP-----BPCTYGSATPVLGSP-----S 74
Db 299 CLNDGRCIDL-----VNGYQCNCQPGTSLGNCINFPDCCASNPCMHGVCDVGINRYSCVCS 354

Qy 75 PDGAG-----DPAFSPNIR-----PPFGTWPTGTFSLIIEALHTDSD 112
Db 355 PGFTGQRNIIDICASNPCRKAGATCINDVNGFRICPEGPHHPSCYSQVNECL----- 408

Qy 113 DLTENPERLISRLTORHLVGEWSQDLHSSGRTDLYSRFYRCDHYHYGEGCSV-----FC 167
Db 409 ---SNP-----CHGNTGGLSGYKCLCDAGWGVNCEVDKNECLS 446

Qy 168 RPRDDFGHTCG---RGEKC---PGWKGQYC-----TPIC 196
Db 447 NPCQNGG---TCNNLVNGYRCTCKGFGKYNQVNIDECASNPCLNQGTCPDDVSGYTCHC 504

Qy 197 -----LPGCDHGGCDKGECK-----CRVWGQRYC-----DECTIRYP 229
Db 505 MLPYTGKNCQTVLAPCSNPENCAAVKEAPNFESFSLCLCAPGHWQGRKCTVDVDECISKP 564

Qy 230 GCVHGTG---QQPWOCNCOEGWGLFCNQDLNYCTHHKPC---NGATCTNTGSGSYTCSCR 285
Db 565 CMNNGVCHNTGSGYCECPGPGFSGHDEEDINDCLAN---PCQNGSCVD---HVNFTSCQCHP 622

Qy 286 GYTG---CE---BEC---PCKN---GSCTDLESS---CTCPGFGYK---KCELSAMTCADGCPFNG 333
Db 623 GFIDGKQCTDMNECLSBCKNGGTCSDYVSYTCTCPAGPHGVHCENNIDECTESSCFNG 682

Qy 334 GRC-----DNP---DGGYC-----CPLG---SGFN 352
Db 683 GTCVDGINSFCLCPVGFTGPFCLHIDNECSSNPLNAGTCDVGLGTGYRVCICPLGYTGKN 742

Qy 353 CEK---KDCS---SPC-----DNP-----DGGYC-----CPLG---SGFN 352
Db 743 CQTLVNLCSRPCNKGTCVQEKARPHCLCPGWDGAYCDVLNVSKAAALQKGVPEHL 802

Qy 363 ---NGACVDLGNSCYCCQAGFG---RC---DNVDDCAS---PC---NGGTCVDND-----SCTCPP 407
Db 803 CQHSICINAGNTHHCQCLPGYTGSYCEEQLDECASNPCQHATC---NDPFGGYRCECV 860

Qy 408 GY---GNKCS---PVSREH---PCHNGATC---HRRYCECAGYGNQCFLPPEPBP----- 453
Db 861 GYQGVNCEYEYDEQNPQCNQGGTCIDLNVHFKSC-----PPGTGLLCEE 907

Qy 454 -VDEEQFPWACAGLVLILLCAAV-----VCVRLKQKPECETETMNNLAN---CQREK 503
Db 908 NIDE-----CAGPHCLNGGQCVDRIIGGYTCRCLPGFAGERCEBGDINECLSNPSCSE- 959

Qy 504 DSSIGATQIKN 514
Db 960 -GSLDCVQLKN 969
  
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RESULT 15
 S18188
 notch protein homolog - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
 R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
 Development 113, 199-205, 1991

A:Title: A homolog of Drosophila Notch expressed during mammalian development.
 A:Reference number: S18188; MUID:92111383; PMID:1764995
 A:Accession: S18188
 A:Molecule type: mRNA
 A:Residues: 1-2531 <WEI>
 A:Cross-references: EMBL:X57405; NID:957634; PID:957635
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 F:987-1018/Domain: EGF homology <EGF1>
 F:1025-1056/Domain: EGF homology <EGF>
 F:1233-1264/Domain: EGF homology <EGF2>
 F:1917-1949/Domain: ankyrin repeat homology <AN1>
 F:1950-1982/Domain: ankyrin repeat homology <AN2>
 F:1984-2016/Domain: ankyrin repeat homology <AN3>
 F:2017-2049/Domain: ankyrin repeat homology <AN4>
 F:2050-2082/Domain: ankyrin repeat homology <AN5>

```

Query Match      14.3%; Score 484.5; DB 2; Length 2531;
Best Local Similarity 27.5%; Pred. No. 3.7e-22;
Matches 189; Conservative 52; Mismatches 208; Indels 239; Gaps 47;

Qy 11 CVSGVFELKLOEFVVK---KGLLRNC-----CRGGGCC-----TFPRVCLKHQY 52
Db 505 CVD-----KINEFLCQCPKPSGHLCOYDVECASTPCCKGAKCLDGPNTVTCVTEGYT 559

Qy 53 AS-----VSPEPPCTYGSATPVLGFS-----PDGAG-----DPAFSPNIRPFEPG 93
Db 560 GTHCEVDIDCEDPD---PCHIGLCKDGVATFTCLQPGYTGHHCTNINECHSQPCRGGTC 618

Qy 94 TWPCTFSLIIEALHTDSP-----DLTENPERLISRLTORHLVGEWSQDLHSSGR---T 145
Db 619 QDRDNYVCLCLKGTGTGPNCEINLDDCASNP-----CDSGTCLD 657

Qy 146 DLVSYRVCDEHYHYGEGCSV-----FCRPRDDFGHTCG----- 179
Db 658 KIDGYECACBPGYTGSMCNVINIDECAGSPCHNGTC---EDGIAGTFCRCPGYHDPCTCLS 715

Qy 180 -----RGEKC---PGWKGQYCTPICLPQCQDQHGCDKPECK----- 212
Db 716 EVNECSNPICIHGACRDGLNGYKCDCAPGWSGTNC---DINNNECESNFCVNGGTCKDMTSG 774

Qy 213 ---CRVWGQRYC---DECIRYPGCVHGTG----- 236
Db 775 YVCTCREGFGSPNQTNINECASNPCLNQGTCTDDVAGYKCNCLPYTGATCEVVLAPCA 834

Qy 237 -----QQPWOCNCOEGWGLFCNQDLNYCTHHKPC---NGATCTNTGSGSYT 280
Db 835 TSPCKNSGVKESEDYSEFSVCVPTGQGTCEIDINECV---KSPCRHGASCQNT---NGSYR 892

Qy 281 CSCRPGYTG---CE---BEC---PCKN---GSCTDLESS---CTCPGFGYK---CELSAMTCADG 328
Db 893 CLCQAGYTGNCESDIDDCRPNFCHNGSGCTDGVNAAFCDCLPGFQGAFCCEEDINECATN 952

Qy 329 PCFNGGRCDNPDDGGYCCPLGSGFN---CEKK---DCS---SPC---NGACVDLGNYS---CCQAG 378
Db 953 PCQNGANCTCDVDSYTCCTCTGTFGHCENNTPDCTESSCFNGGTCVDGINSFTCLCPPG 1012

Qy 379 F---GRCD---NVDDCAS---PC---NGGTCVDND-----CTCPGY---GNKCSVSR---CBH---PCHN 425
Db 1013 FTGSYCYQDVNECDSPRLHGGTC---QDSYGTCTCPOGTTGLNQNVLWVCDASAPCKN 1070

Qy 426 GATCHRR-----YCEC---AGYGG---NCQFLLPPEPVPVDEQFPWAYCA---GLVLLLLGCAA 476
Db 1071 GKKCWQNTQYHCECRSGWTGFNCVL-----SVSCEVAAKRGIDVTLCCQHG 1119

Qy 477 VCVRLKQKPECETETMNNLANCQREK 504
Db 1120 GLCVDBEDKHCHYCCQAGYTGSGYCEDEVD 1147
  
```

Search completed: November 29, 2004, 13:27:05
 Job time : 17.4855 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:12:09 ; Search time 69.5872 Seconds
(without alignments)
4779.132 Million cell updates/sec

Title: US-09-783-931-13
Perfect score: 3383
Sequence: 1 MGRLLASALLCVSGVFELK.....DTKYQSVVSEKDECIATEV 578

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_eprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	73.6	728	2 Q90656	Q90656 gallus gall
2	2466	72.9	722	2 D1L1 MOUSE	Q61483 mus musculus
3	2466	72.9	722	2 Q6PFV7	Q6PFV7 mus musculus
4	2466	72.9	722	2 AAH57400	AAH57400 mus musculus
5	2466	72.9	722	2 AAR30869	AAR30869 mus musculus
6	2466	72.9	722	2 AAH65063	AAH65063 mus musculus
7	2436	72.0	714	1 D1L1 RAT	P97677 rattus norv
8	2401.5	71.0	723	1 D1L1 HUMAN	O00548 homo sapien
9	2267.5	67.0	726	2 Q8AW87	Q8AW87 cynops pyrr
10	2262.5	66.9	721	2 Q91902	Q91902 xenopus lae
11	2084.5	61.6	720	2 Q8UW44	Q8UW44 brachydanio
12	2081.5	61.5	717	2 P87357	P87357 brachydanio
13	2014	59.5	772	2 Q6DI48	Q6DI48 brachydanio
14	1989.5	58.8	802	2 Q57462	Q57462 brachydanio
15	1383	40.9	642	2 Q7ZXT4	Q7ZXT4 xenopus lae
16	1377	40.7	642	2 P79941	P79941 xenopus lae
17	1349	39.9	664	2 Q91A16	Q91A16 brachydanio
18	1338.5	39.6	615	2 Q57409	Q57409 brachydanio
19	1329.5	39.3	685	1 D1L4 HUMAN	Q9NR61 homo sapien
20	1301.5	38.5	686	1 D1L4 MOUSE	Q91J17 mus musculus
21	1298.5	38.4	686	2 Q9DBJ9	Q9DBJ9 mus musculus
22	1197.5	35.4	684	2 Q81498	Q81498 cupiennius
23	1086.5	32.1	833	1 D1L DROME	P10041 drosophila
24	1086.5	32.1	833	2 Q6T4M9	Q6T4M9 drosophila
25	1086.5	32.1	833	2 Q6T4N0	Q6T4N0 drosophila
26	1086.5	32.1	833	2 Q6T4N1	Q6T4N1 drosophila
27	1086.5	32.1	833	2 Q6T4N2	Q6T4N2 drosophila
28	1086.5	32.1	833	2 Q6T4N3	Q6T4N3 drosophila
29	1086.5	32.1	833	2 Q6T4N4	Q6T4N4 drosophila
30	1086.5	32.1	833	2 Q6T4N6	Q6T4N6 drosophila
31	1086.5	32.1	833	2 AAO25024	AAO25024 drosophila

ALIGNMENTS

RESULT 1

ID	Q90656	PRELIMINARY;	PRT;	728 AA.
AC	Q90656;			
DT	01-NOV-1996	(Tremblrel. 01, Created)		
DT	01-NOV-1996	(Tremblrel. 01, Last sequence update)		
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)		
DE	C-Delta-1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spinal cord;			
RX	MEDLINE=95319507; PubMed=7596411;			
RA	Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowitz D.;			
RT	"Expression of a Delta homologue in prospective neurons in the chick."			
RL	Nature 375:787-790(1995).			
DR	EMBL; U26590; AAC59689.1; -.			
DR	PIR; I50719; I50719.			
DR	HSSP; P00740; IEDM.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0007154; P:cell communication; IEA.			
DR	InterPro; IPR000152; AaX_hydroxyl_S.			
DR	InterPro; IPR001774; DSL.			
DR	InterPro; IPR000742; EGF 2.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR001438; EGF-II.			
DR	InterPro; IPR006209; EGF_like.			
DR	Pfam; PF01414; DSL; 1.			
DR	Pfam; PF00008; EGF; 6.			
DR	PRINTS; PR00010; EGFBL00D.			
DR	SMART; SM00051; DSL; 1.			
DR	SMART; SM00179; EGF_CA; 4.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.			
DR	PROSITE; PS00022; EGF_1; 8.			
DR	PROSITE; PS01186; EGF_2; 8.			
DR	PROSITE; PS00026; EGF_3; 6.			
DR	PROSITE; PS01187; EGF_CA; 2.			
KW	EGF-like domain.			
SQ	SEQUENCE 728 AA; 79861 MW; 93BD2D6666D2388B7 CRC64;			

Query Match 73.6%; Score 2489; DB 2; Length 728;

Best Local Similarity 76.0%; Pred. No. 7.3e-174;

Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

Qy 5 LASALLC-----VSGVFELKQSFVNKKGLL--NRNCCRGCG-----CCTFFRVCL 48

Db 11 LLSALLRCQVDSGVFELKQSFVNKKGLLSNRNCCRGCGGGAGGAGGQCCCKTFFRVCL 70

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QY 49 KHYQASVPEPCTYGSA--TPVLG--SFS-PDGAG--DPAFNPPIRPFPGFTWPGTFSLI 102
DB 71 KHYQASVPEPCTYGSAITPVLGANSFVDPGAGGADPAFNPPIRPFPGFTWPGTFSLI 130
QY 103 IEALHTDSPDDL--TENPERLISRL--TORHL--VGEEMSQDLHSSGRDLD--YSYRFVCDHY 158
DB 131 IEALHTDSPDDL--TENPERLISRL--TORHL--VGEEMSQDLHSSGRDLD--YSYRFVCDHY 190
QY 159 YGEGSVFCRPRD--FGHTCG--RGRK--C-PGWKGQYCT--PICLPD--OHG--CDKPGBC 211
DB 191 YGEGSVFCRPRD--FGHTCG--RGRK--C-PGWKGQYCT--PICLPD--OHG--CDKPGBC 250
QY 212 KCRVHGQGRYCDICRYPCGVHGTCTOOPWQCNCOEGWGLFCNODLNYCTHHKPC--NGAT 270
DB 251 KCRVHGQGRYCDICRYPCGVHGTCTOOPWQCNCOEGWGLFCNODLNYCTHHKPC--NGAT 310
QY 271 CNTNGGSGYTCSCRPYGTG--CE--EEC--PCKN--GSCDTLES--SCTCPGFGYK--C 318
DB 311 CNTNGGSGYTCSCRPYGTGSSCEIEINECDANPCKN--GSCDTLESYSCTCPGFGYKNC 370
QY 319 ELSAMTCADGCPNGRC--DNDPGY--C-CPLG--SGFNCEKK--DCSSPC--NGA--CVDL 369
DB 371 ELSAMTCADGCPNGRC--DNDPGY--C-CPLG--SGFNCEKK--DCSSPC--NGA--CVDL 430
QY 370 GNSY--C-COAG--GR--C-DNVD--CAS--PC--NGTCD--VND--SCTCPGY--GNCS--PVS 417
DB 431 GNSY--C-COAG--GR--C-DNVD--CAS--PC--NGTCD--VND--SCTCPGY--GNCS--PVS 490
QY 418 RCEH--PCHNGATCHRR--YCECA--GYGG--NCOFL--PEPP--GPV-----DERQ 458
DB 491 RCEH--PCHNGATCHRR--YCECA--GYGG--NCOFL--PEPP--GPV-----DERQ 550
QY 459 FPH--AVCAGLVL--LLGCA--VVCRLK--OKPEC--ETETMNLANCOREKD--504
DB 551 FPH--AVCAGLVL--LLGCA--VVCRLK--OKPEC--ETETMNLANCOREKD--504
QY 505 --SSICATQIKNTKK--DFH--DK--KVRYP--VDYNLV--KV-----HKKC---541
DB 611 SISVIGATQIKNTKKVDFHSDNSDRKNGYKVRYPVDYNLVHKLKNEKNSVKEHGKCEAK 670
QY 542 -----SBEKAL-----RKRP--SVYSTSKDTKYQSVVV--SEKDEC--IATEV 578
DB 671 CETYDSEAEKSAVLKSSDTSERKRPDSVYSTSKDTKYQSVVISEKDECIATEV 728

RESULT 2
DL11 MOUSE
ID DL11 MOUSE STANDARD; PRT; 722 AA.
AC O614E3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
GN Names=Dll1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;
RX MEDLINE=95401858; PubMed=7671805;
RA Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
RT "Transient and restricted expression during mouse embryogenesis of
RT Dll1, a murine gene closely related to Drosophila Delta.";
RL Development 121:2407-2418(1995).
CC -!- FUNCTION: May be involved in cell-to-cell communication in
CC mammalian embryos. May have a role in cellular interactions
CC underlying somitogenesis and development of the nervous system.
CC -!- SUBUNIT: Interacts with Notch receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In the embryo, expressed in the paraxial
CC mesoderm and nervous system. Expressed at high levels in adult
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FT DISULFID 331 342 By similarity.
FT DISULFID 336 351 By similarity.
FT DISULFID 353 362 By similarity.
FT DISULFID 369 380 By similarity.
FT DISULFID 374 390 By similarity.
FT DISULFID 392 401 By similarity.
FT DISULFID 408 419 By similarity.
FT DISULFID 413 428 By similarity.
FT DISULFID 430 439 By similarity.
FT DISULFID 446 466 By similarity.
FT DISULFID 468 477 By similarity.
FT DISULFID 484 495 By similarity.
FT DISULFID 489 504 By similarity.
FT DISULFID 506 515 By similarity.
FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 722 AA; 78448 MW; 95F581B56DEC9B0 CRC64;

Query Match 72.9%; Score 2466; DB 1; Length 722;
Best Local Similarity 76.6%; Pred. No. 3.5e-172;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

Qy 1 MGR-----LLASALLC---VSGVFELKLOEFVNKKGLL--NRNCCRGG-----GCCTFFR 45
Db |||
1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLNRNCCRGSGSPPCACRTFFR 60
Qy 46 VCLKHYQASVPEPPCTYGSA--TPVLG--SFS--PDGAG--DPAFNSNPIRFPFGFTWPGTFS 100
Db |||
61 VCLKHYQASVPEPPCTYGSATVPLGVDSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFS 120
Qy 101 LIIIALHTSDPDDL--TENPERLISRL--TORHL--VGEWSQDLHSGRTDL--YSRFPVCDE 156
Db |||
121 LIIIALHTSDPDDL--TENPERLISRL--TORHL--VGEWSQDLHSGRTDL--YSRFPVCDE 180
Qy 157 HYEGEGSVFCRPRDD--FGHFTCG--RGEK--C--PGWKGOYCT--PICLPCC--DOHG--CKPG 209
Db |||
181 HYEGEGSVFCRPRDDAFHFTCGDGRGKMDPGWKGOYCTDPICLPCDDQHGKCKPG 240
Qy 210 ECKCRVGMQGRYCDICIRYPCVHGTCCQPCQWQCQEGWGLFCNQDLNLYCTHHKPC--NG 268
Db |||
241 ECKCRVGMQGRYCDICIRYPCVHGTCCQPCQWQCQEGWGLFCNQDLNLYCTHHKPCRN 300
Qy 269 ATCTNTGSGSYTCSCRGYTG--CE-----EEC--PKNG--SCTDLES--SCTCPGPGYK 317
Db |||
301 ATCTNTGSGSYTCSCRGYTGANCELEVEDECAPSPCKNGASCTDLESFSCTCPGPGYK 360
Qy 318 -CELSAMTCADGCFNGRC--DNPDDGY--C--CPLG--SGFNCEKXD--C--SSPC--NGA--CV 367
Db |||
361 VCELSAMTCADGCFNGRCSDNPDGTYCHCPLGSGFNCEKXKQDLGSSPCNGAKCV 420
Qy 368 DLGNSY--C--COAGF--GR--C--DNVDDCA--SPC--NGGTC--DYND--SCTCPGY--GKNGS--P 415
Db |||
421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCTCRDSVNDFSCTCPGYTGKNCAP 480
Qy 416 VSRCEH--PCNGATCHRR-----YCECA--GYGG--NQFLLP--PPGP--VD-----BEQ- 458
Db |||
481 VSRCEHAPCHNGATCHORQGRYMCACQGYGPNCCQLLPPPPGPMVVDLSERHMSQ 540
Qy 459 --PPW--AVCAGLV--L--LLLLGCA--VVCVRLK--OK-----KVRYP--VDNVLV--LK-----VHKK 540
Db |||
541 GPFPWAVCAGVLVLLLLGCAAVVCVRLKQKHQPPPPGPGGETETMNNLANCQREK 600
Qy 504 D---SSIGATQIKNTKK--DFHDK-----KVRYP--VDNVLV--LK-----VHKK 540
Db |||
601 DVSVSIIGATQIKNTKKADPHGAKSKSFYRPTVDVNLVLDLKGDEATVDRTHSK 660
Qy 541 -----CSEKAL-----RKRP--SVYSTSKTKYQSVVY--SEKDEK--IAT 576
Db |||
661 RDTKCQSQSAGEEKIAPTLLRGIBPDKRPESVYSTSKTKYQSVVYLSAEKDECVIAT 720
Qy 577 EV 578
Db |||
721 EV 722

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RESULT 3
O6PFV7
ID O6PFV7 PRELIMINARY; PRT; 722 AA.
AC O6PFV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Delta-like 1.
GN Name=Dll1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Nagaraja R., Waeltz P., Brathwaite M.E.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; BC057400; AAH57400.1; -.
DR EMBL; AY497019; AAR30869.1; -.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.
DR GO; GO:0001757; P:somite specification; IMP.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR01436; EGF_II.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.

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DR Pfam: PF01414; DSL; 1.
DR Pfam: PF00008; EGF; 6.
DR Pfam: PF07645; EGF_CA; 1.
DR PRINTS: PR00010; EGFBL00D.
DR SMART: SM00051; DSL; 1.
DR SMART: SM00181; EGF; 8.
DR SMART: SM00179; EGF_CA; 6.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; 8.
DR PROSITE: PS01186; EGF_2; 8.
DR PROSITE: PS00026; EGF_3; 6.
DR PROSITE: PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match
Best Local Similarity 72.9%; Score 2466; DB 2; Length 722;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY 1 MGR-----LLASALLC---VSGVPELKLQEFVNKKGLL-NRNCRRG-----GCCTFFR 45
DB : |||||
DB 1 MGRRSALALAVSALLCQVWSSGVPELKLQEFVNKKGLLGNRNCRRGSGPPCACRTPFR 60
QY 46 VCLKHQYQASVSEPPCTCYGSA--TPVLG--SFS-PDGAG-DPAFSPNIRPFPGFTWPGTFS 100
DB |||||
DB 61 VCLKHQYQASVSEPPCTCYGSAVTPVLGVDSFSLPDGAGIDPAFSPNIRPFPGFTWPGTFS 120
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TORHL-VGEWSODLHSSGRTDL-VSYRPFVCD 156
DB |||||
DB 121 LIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSODLHSSGRTDLRYSYRPFVCD 180
QY 157 HYYGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DQHG-CDKPG 209
DB |||||
DB 181 HYYGEGSVFCRPRDDAFGHFTCGRGEKMCDPGWKGOYCTDPICLPGCCDQHGCDKPG 240
QY 210 ECKRVGWQGRYCDCEIRYPGCVHGTCTQOPWQCNQEGWGLFCNQDLNYCTHHKPC-NG 268
DB |||||
DB 241 ECKRVGWQGRYCDCEIRYPGCLHGTCTQOPWQCNQEGWGLFCNQDLNYCTHHKPC-NG 300
QY 269 ATCTNTGQSYTCSRPGVTG--CE---BEC---PCNKG-SCTDLES--SCTCPPGFYGK 317
DB |||||
DB 301 ATCTNTGQSYTCSRPGVTGANCELEVDCAFSPCKNGASCTDLESFSCCTPPGPHYGK 360
QY 318 -CELSAMTCADGCFNCGRC-DNPDGGY-C-CPLG-SGFNCKKD--C-SSPC-NGA-CV 367
|||

Query Match
Best Local Similarity 72.9%; Score 2466; DB 2; Length 722;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY 1 MGR-----LLASALLC---VSGVPELKLQEFVNKKGLL-NRNCRRG-----GCCTFFR 45
DB : |||||
DB 1 MGRRSALALAVSALLCQVWSSGVPELKLQEFVNKKGLLGNRNCRRGSGPPCACRTPFR 60
QY 46 VCLKHQYQASVSEPPCTCYGSA--TPVLG--SFS-PDGAG-DPAFSPNIRPFPGFTWPGTFS 100
DB |||||
DB 61 VCLKHQYQASVSEPPCTCYGSAVTPVLGVDSFSLPDGAGIDPAFSPNIRPFPGFTWPGTFS 120
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TORHL-VGEWSODLHSSGRTDL-VSYRPFVCD 156
DB |||||
DB 121 LIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSODLHSSGRTDLRYSYRPFVCD 180
QY 157 HYYGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DQHG-CDKPG 209
DB |||||
DB 181 HYYGEGSVFCRPRDDAFGHFTCGRGEKMCDPGWKGOYCTDPICLPGCCDQHGCDKPG 240
QY 210 ECKRVGWQGRYCDCEIRYPGCVHGTCTQOPWQCNQEGWGLFCNQDLNYCTHHKPC-NG 268
DB |||||
DB 241 ECKRVGWQGRYCDCEIRYPGCLHGTCTQOPWQCNQEGWGLFCNQDLNYCTHHKPC-NG 300
QY 269 ATCTNTGQSYTCSRPGVTG--CE---BEC---PCNKG-SCTDLES--SCTCPPGFYGK 317
DB |||||
DB 301 ATCTNTGQSYTCSRPGVTGANCELEVDCAFSPCKNGASCTDLESFSCCTPPGPHYGK 360
QY 318 -CELSAMTCADGCFNCGRC-DNPDGGY-C-CPLG-SGFNCKKD--C-SSPC-NGA-CV 367
|||

Query Match
Best Local Similarity 76.6%; Pred. No. 3.5e-172;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY 1 MGR-----LLASALLC---VSGVPELKLQEFVNKKGLL-NRNCRRG-----GCCTFFR 45
DB : |||||
DB 1 MGRRSALALAVSALLCQVWSSGVPELKLQEFVNKKGLLGNRNCRRGSGPPCACRTPFR 60
QY 46 VCLKHQYQASVSEPPCTCYGSA--TPVLG--SFS-PDGAG-DPAFSPNIRPFPGFTWPGTFS 100
DB |||||
DB 61 VCLKHQYQASVSEPPCTCYGSAVTPVLGVDSFSLPDGAGIDPAFSPNIRPFPGFTWPGTFS 120
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TORHL-VGEWSODLHSSGRTDL-VSYRPFVCD 156
DB |||||
DB 121 LIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSODLHSSGRTDLRYSYRPFVCD 180
QY 157 HYYGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DQHG-CDKPG 209
DB |||||
DB 181 HYYGEGSVFCRPRDDAFGHFTCGRGEKMCDPGWKGOYCTDPICLPGCCDQHGCDKPG 240
QY 210 ECKRVGWQGRYCDCEIRYPGCVHGTCTQOPWQCNQEGWGLFCNQDLNYCTHHKPC-NG 268
DB |||||
DB 241 ECKRVGWQGRYCDCEIRYPGCLHGTCTQOPWQCNQEGWGLFCNQDLNYCTHHKPC-NG 300
QY 269 ATCTNTGQSYTCSRPGVTG--CE---BEC---PCNKG-SCTDLES--SCTCPPGFYGK 317
DB |||||
DB 301 ATCTNTGQSYTCSRPGVTGANCELEVDCAFSPCKNGASCTDLESFSCCTPPGPHYGK 360
QY 318 -CELSAMTCADGCFNCGRC-DNPDGGY-C-CPLG-SGFNCKKD--C-SSPC-NGA-CV 367
|||
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Db 361 VCELSAMTCADGPGCFNGRCSDNPDGGYTHCPILGFSGFCNCKMDLGGSPCSNGAKCV 420
Qy 368 DLGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTPPGY-GKNC-S-P 415
Dd 421 DLGNSYLCRCOAGSGRVCEDNVDDCASSPANGGTCDSDVNDPSCCTPPGYTKNC-SAP 480
Qy 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----BEQ- 458
Dd 481 VSRCEHAPCHNGATCHORQORYMCECAQGYGPNCCQFLLPBPFGPMVVDLSERHMSQ 540
Qy 459 --FPW-AVCAGLV--LILLGCAA-VVCVRLK-OK-----PE-C--ETETMNNLANCOREK 503
Dd 541 GPFPPWAVACAGVLVLLLLGCAA-VVCVRLKOKHQHPPPCGGTETMNNLANCOREK 600
Qy 504 D---SSIGATQIKNTKK-DPHDK-----KVRYP-VDYNLV--LK-----VHKK 540
Dd 601 DVSVIIGATQIKNTKKADPHDGAESKSFVRYPTVDYNLVRLDLKGDEATVRDTHSK 660
Qy 541 -----CSEKAL-----RKRP-SVYSTSKOTKYOSVVY--SEKDEC-IAT 576
Dd 661 RDKCQSSSAGEEKIAPTLLRGGEIPDKRPESVYSTSKOTKYOSVVYLSAEKDECVIAT 720
Qy 577 EV 578
Dd 721 EV 722

RESULT 5
AAR30869
ID AAR30869 PRELIMINARY; PRT; 722 AA.
AC AAR30869;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Delta-like-1.
GN DLI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Brathwaite M., Waeltz P., Brathwaite M.E.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY497019; AAR30869.1;
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7BEC75E CRC64;

Query Match 72.9%; Score 2466; DB 2; Length 722;
Best Local Similarity 76.6%; Pred. No. 3.5e-172;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

Qy 1 MGR-----LLASALLC---VSGVFELKQEFVNNKGLL-NRNCRCGG-----GCCTFFR 45
Dd 1 MGRSALALAVSALLCOVWSSGFFELKQEFVNNKGLLNRNCRCGGSGPPACRTFFR 60
Qy 46 VCLKHYQASVSPPECTYGS-A-TPVLG--SFS-PDGAG-DPAPSNPIRFFPGFTWPTFS 100
Dd 61 VCLKHYQASVSPPECTYGS-A-TPVLG--SFS-PDGAG-DPAPSNPIRFFPGFTWPTFS 120
Qy 101 LIIBALHTDSDDL-TENPERLISRL-TQRHL-VGEWSDQLHSSGRTDL-YSYRFFVDE 156
Dd 121 LIIBALHTDSDDL-TENPERLISRL-TQRHL-TGEWSDQLHSSGRTDLRYSYRFFVDE 180
Qy 157 HYEGGGSVCRRPDD--FGHTCG-RGEK-C-PGWKQYCT-PICLPGC-DQHG-CDKPG 209
Dd 181 HYEGGGSVCRRPDDAFGHFTCGDRGKMDPGWKGQYCTDPICLPGCDQHGCDKPG 240

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Qy 210 ECKRVGMOGRYCDCEIRYPCVHGTQQPQMCNCQBGWGLFCNQDLNYCTHHKPC-NG 268
Dd 241 ECKRVGMOGRYCDCEIRYPCVHGTQQPQMCNCQBGWGLFCNQDLNYCTHHKPC-RNG 300
Qy 269 ATCTNTQGSYTCSCRPYTG--CE-----BEC--PCXNG-SCTDLES--SCTCPGPGYVK 317
Dd 301 ATCTNTQGSYTCSCRPYTGANCELEVEDCAPSPCKNGASCTDLEPSFSCCTCPGPGYVK 360
Qy 318 -CELSAMTCADGPGCFNGRC-DNPDGGY-C-CPLG-SGFNCEKDD--C-SSPC-NGA-CV 367
Dd 361 VCELSAMTCADGPGCFNGRCSDNPDGGYTHCPILGFSGFCNCKMDLGGSPCSNGAKCV 420
Qy 368 DLGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTPPGY-GKNC-S-P 415
Dd 421 DLGNSYLCRCOAGSGRVCEDNVDDCASSPANGGTCDSDVNDPSCCTPPGYTKNC-SAP 480
Qy 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----BEQ- 458
Dd 481 VSRCEHAPCHNGATCHORQORYMCECAQGYGPNCCQFLLPBPFGPMVVDLSERHMSQ 540
Qy 459 --FPW-AVCAGLV--LILLGCAA-VVCVRLK-OK-----PE-C--ETETMNNLANCOREK 503
Dd 541 GPFPPWAVACAGVLVLLLLGCAA-VVCVRLKOKHQHPPPCGGTETMNNLANCOREK 600
Qy 504 D---SSIGATQIKNTKK-DPHDK-----KVRYP-VDYNLV--LK-----VHKK 540
Dd 601 DVSVIIGATQIKNTKKADPHDGAESKSFVRYPTVDYNLVRLDLKGDEATVRDTHSK 660
Qy 541 -----CSEKAL-----RKRP-SVYSTSKOTKYOSVVY--SEKDEC-IAT 576
Dd 661 RDKCQSSSAGEEKIAPTLLRGGEIPDKRPESVYSTSKOTKYOSVVYLSAEKDECVIAT 720
Qy 577 EV 578
Dd 721 EV 722

RESULT 6
AAH65063
ID AAH65063 PRELIMINARY; PRT; 722 AA.
AC AAH65063;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Delta-like-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilek F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065063; AAH65063.1; -.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match      72.9%; Score 2466; DB 2; Length 722;
Best Local Similarity 76.6%; Pred. No. 3.5e-172;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY 1 MGR-----LLASALIC---VSGVRELKLOEFVNKGLL-NNCCRGG-----GCTTFR 45
Db 1 MGRSALALAVSALLCQWSSGVFELKLOEFVNKGLLNNCCRGSGGPPCACTTFR 60
QY 46 VCLKHQAQSVPEPCTYGS-TPVLG--SFS-PDGAG-DPAFNSNIRPFPGFTWPGTFS 100
Db 61 VCLKHQAQSVPEPCTYGS-TPVLG--SFS-PDGAG-DPAFNSNIRPFPGFTWPGTFS 120
QY 101 LIIEALHTSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSGRTDL-YSYRPFVDE 156
Db 121 LIIEALHTSPDDL-TENPERLISRL-TQRHLTVGEWSQDLHSGRTDLRYSYRPFVDE 180
QY 157 HYEGECVFCRPRD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DOHG-CDKEG 209
Db 181 HYEGECVFCRPRD-DAFHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DOHG-CDKEG 240
QY 210 ECKCRVGMQGRYDECIRYPGVGHGTCQOPWCNCOEGWGLFCNODLNYCTHHKPC-NG 268
Db 241 ECKCRVGMQGRYDECIRYPGVGHGTCQOPWCNCOEGWGLFCNODLNYCTHHKPC-NG 300
QY 269 ATCTNTGQSGYTCSCRPGYTG--CE---BEC---PCXNG-SCTDLES--SCTCPGPFYK 317
Db 301 ATCTNTGQSGYTCSCRPGYTG--CE---BEC---PCXNG-SCTDLES--SCTCPGPFYK 360
QY 318 -CELSAMTCADGCFNGRC-DNPDGY-C-CPLG-SGFNCERKD--C-SSPC-NGA-CV 367
Db 361 VCELSAMTCADGCFNGRC-DNPDGY-C-CPLG-SGFNCERKD--C-SSPC-NGA-CV 420
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SFC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415
Db 421 DLGNSYLCRCQAGFSRYCEDVDDCASSPCANGGTCRDSVNDVDFCTCPGYTKNCSAP 480
QY 416 VSRCEH-PCNHGATCHRR-----YCECA-GYGG-NCQFLPE-PPGP--VD-----EQ- 458
Db 481 VSRCEHAPCHGATCHQRQRYMCECAQGYGPNCOFLPEPPPGPMVVDLSERHMSQG 540
QY 459 --FPW-AVCAGLV--LALLGAA-VVCYRLK-QK---PE-C--ETETMNNLNCOREK 503
Db 541 GPFPPVAVCAGVVLVLLLLGAAVVCYRLKQKHPPEPCGGTETMNNLNCOREK 600
QY 504 D---SSIGATQKNTKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540
Db 601 DVSVSIIIGATQKNTKKADFGHGAERKSSFKVRYPTVDYNLVRLDKGDEATVRDTHSK 660
QY 541 -----CSEKAL-----RKRP-SVTSKDTKYQSVYV--SEKDEC-IAT 576
Db 661 RDTKQSQSSAGEEIKIAPTIRGGEIPDRKRPSVYSTSKDTKYQSVYVLSAEKDECVIAT 720
QY 577 EV 578
Db 721 EV 722

RESULT 7
DL1L1 RAT
AC F97677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE GN OS OC OX RN RP RA
Name=D111;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
Disbio G., Hebshi L., Boulter J., Weinmaster G.;
Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
!- FUNCTION: May be involved in cell-to-cell communication in
mammalian embryos. May have a role in cellular interactions
underlying somitogenesis and development of the nervous system (By
similarity).
!- SUBUNIT: Interacts with Notch receptors.
!- SUBCELLULAR LOCATION: Type I membrane protein.
!- SIMILARITY: Contains 1 DSL domain.
!- SIMILARITY: Contains 8 EGF-like domains.
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EMBL; U78889; AAB37343.1; -.
HSP; P08709; 1BF9.
RGD; 70949; D11.
GO; GO:0005576; C:extracellular; ISS.
GO; GO:0005887; C:integral to plasma membrane; ISS.
GO; GO:0005111; P:Notch binding; IPI.
GO; GO:0030154; P:cell differentiation; ISS.
GO; GO:0001709; P:cell fate determination; ISS.
GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
GO; GO:0009912; P:hair cell fate commitment; NAS.
GO; GO:0030097; P:hemoiesis; ISS.
GO; GO:0042472; P:inner ear morphogenesis; ISS.
GO; GO:0007399; P:neurogenesis; NAS.
GO; GO:0007219; P:Notch signaling pathway; NAS.
GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
GO; GO:0030155; P:regulation of cell adhesion; ISS.
InterPro; IPR00152; Asx_hydroxyl_S.
InterPro; IPR001774; DSL.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001438; EGF II.
InterPro; IPR006209; EGF_like.
Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 6.
PRINTS; PR00010; EGFLOOD.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF CA; 4.
PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00022; EGF_1; 8.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS00026; EGF_3; 7.
PROSITE; PS01187; EGF CA; 2.
Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
Repeat; Signal; Transmembrane.
SIGNAL 1 17
CHAIN 18 714
DOMAIN 18 537
EXTRACELLULAR (Potential).
FT DOMAIN 538 560
Potential.
FT DOMAIN 561 714
Cytoplasmic (Potential).
FT DOMAIN 158 220
DSL.
FT DOMAIN 225 253
EGF-like 1.
FT DOMAIN 256 284
EGF-like 2.
FT DOMAIN 291 324
EGF-like 3.
FT DOMAIN 331 362
EGF-like 4.
FT DOMAIN 369 401
EGF-like 5.
FT DOMAIN 408 439
EGF-like 6.
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FT	DOMAIN	446	EGF-like 7, calcium-binding (Potential).	477
FT	DOMAIN	484	EGF-like 8.	515
FT	DISULFID	225	By similarity.	236
FT	DISULFID	229	By similarity.	242
FT	DISULFID	244	By similarity.	253
FT	DISULFID	256	By similarity.	267
FT	DISULFID	262	By similarity.	273
FT	DISULFID	275	By similarity.	284
FT	DISULFID	291	By similarity.	303
FT	DISULFID	297	By similarity.	313
FT	DISULFID	315	By similarity.	324
FT	DISULFID	331	By similarity.	342
FT	DISULFID	336	By similarity.	351
FT	DISULFID	353	By similarity.	362
FT	DISULFID	369	By similarity.	380
FT	DISULFID	374	By similarity.	390
FT	DISULFID	392	By similarity.	401
FT	DISULFID	408	By similarity.	419
FT	DISULFID	413	By similarity.	428
FT	DISULFID	430	By similarity.	439
FT	DISULFID	446	By similarity.	466
FT	DISULFID	468	By similarity.	477
FT	DISULFID	484	By similarity.	495
FT	DISULFID	489	By similarity.	504
FT	DISULFID	506	By similarity.	515
FT	CARBOHYD	476	N-linked (GlcNAc...) (Potential).	476
SQ	SEQUENCE	714 AA;	488EE2272BAEA27E CRC64;	714 AA;
Query Match 72.0%; Score 2436; DB 1; Length 714;				
Best Local Similarity 75.4%; Pred. No. 5.4e-170;				
Matches 538; Conservative 11; Mismatches 29; Indels 136; Gaps 66;				
Qy	1	MGR-----LIASALLC---	VSGVFELKLOFVNKKGLL-NRNCRCG	-----GCCTFFR 45
Db	1	MGRSALALAVVSALLCQVWSSGVFELKLOFVNKKGLLGNRCGSGSPPCACRFFR	60	
Qy	46	VCLKHQASVSPPECTYGS-A	TPVLG--SFS-PDGAG-DPAFNP	IRFPFGFTWPGTFS 100
Db	61	VCLKHQASVSPPECTYGS-A	TVLGVDSFSLPDGAGIDPAFNP	IRFPFGFTWPGTFS 120
Qy	101	LIIEALHTDSPDDL-TENPERLISRL-TORHL-VGEESQDLHSSGRDIL-VSYRFV	CDL 156	
Db	121	LIIEALHTDSPDDL-TENPERLISRL-TORHLTVGEESQDLHSSGRDILSYRFV	CDL 180	
Qy	157	HYEGGCVFCRPRDD-FGHFTCG-RGEK-C	-PGWKGOYCT-PTCLPGC-DOHG	-CDKPG 209
Db	181	HYEGGCVFCRPRDDAFGHFTCGERGEKCDPWKGOYCTDPICLPGCDQHG	YCDKPG 240	
Qy	210	ECKRVGQGRYCDICIRYPCVHGT	COQWQCNCQEGWGLFCNQDLNYCTHKKPC	-NG 268
Db	241	ECKRVGQGRYCDICIRYPCVHGT	COQWQCNCQEGWGLFCNQDLNYCTHKKPC	300
Qy	269	ATCTNTGGSYTCRCRGYTG--CE---BEC---	PCKN-GSCTDLES--SCTCPGPGYK 317	
Db	301	ATCTNTGGSYTCRCRGYTG--CE---	PCKN-GSCTDLES--SCTCPGPGYK 360	
Qy	318	-CELSAMTCADGCPFGNRC-DNPDGGY-C	-CPLG-SGFNCEKK--DCSSPC-NGA	-CV 367
Db	361	VCELSAMTCADGCPFGNRCSDNPDGGYTHCPAG	FGFNCEKKIDLCSSPFCNGAKCV 420	
Qy	368	DLGNSY-C-CQAGF-GR-C-DNVDCA	-SPC-NGGTC--DYND-SCTCPGPGYK	-GKNGS-P 415
Db	421	DLGNSYLCRCQTFSGRYCEDNVDCCASSPCANGT	CRDSVNDPFCPTGTYGRNCSP 480	
Qy	416	VSRCEH-PCNGATCHRR-----YCECA	-GYGG-NCQFLLPEPPGPV-----DEEOPFW	-AV 463
Db	481	VSRCEHAPCHNGATCHORQRYMCECAQGYG	ANGCQFLLPEPPGPVVA 540	
Qy	464	CAGLV---LILLGCAA-VVCVRLK---	QKP--EC---ETETMNNLANCOREKD---	SSIG 508
Db	541	CAGVLLVLLLGCAAVVVCVRLKQKHQPP	PCGGSETMNNLANCOREKDVSVIIG 600	
Qy	509	ATQIKNTNKK-DFH-----DK---	KVRYP-VQYNLV-----LKVHKKC---	541

Db	601	ATQIKNTNKKADFGHDGADKSSFKARYPTVDYLNIRDLKGDEATVRDAHSKRDTKCSQ	660
Qy	542	---SEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV	578
Db	661	GSVGEKSTLRCGEVDPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIATEV	714
RESULT 8			
DILI1 HUMAN STANDARD; PRT; 723 AA.			
ID	000548; Q9NU41; Q9UUV2;		
AC	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta)		
GN	Name=DILI1; (UNQ146/PRO172).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99180765; PubMed=10079256;		
RA	Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,		
RA	Banks A., Leiman J., Ward D., Ieh-Horowitz D., Artavanis-Tsakonas S.;		
RT	"Human ligands of the Notch receptor.";		
RL	Am. J. Pathol. 154:785-794(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Han W., Ye Q., Moore M.A.S.;		
RT	"A soluble form of human delta-like-1 inhibits differentiation of		
RT	hematopoietic progenitor cells.";		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Oda T., Chandrasekharappa S.C.;		
RT	"Human Delta 1 gene sequence.";		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.";		
RL	Genome Res. 13:2265-2270(2003).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RA	Almeida J.;		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	FUNCTION.		
RX	MEDLINE=21464863; PubMed=11581320;		
RA	Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,		
RA	Henrique D., Parreira L.;		
RT	"Differential effects of Notch ligands Delta-1 and Jagged-1 in human		
RT	lymphoid differentiation.";		
RL	J. Exp. Med. 194:991-1001(2001).		
CC	-I- FUNCTION: Acts as a ligand for Notch receptors. Blocks the		
CC	differentiation of progenitor cells into the B-cell lineage while		
CC	promoting the emergence of a population of cells with the		
CC	characteristics of a T-cell/NK-cell precursor.		
CC	-I- SUBUNIT: Interacts with Notch receptors.		

CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower
 CC expression in brain and muscle and almost no expression in
 CC placenta, lung, liver, and kidney.
 CC -|- SIMILARITY: Contains 1 DSL domain.
 CC -|- SIMILARITY: Contains 8 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF003522; AAB61286.1; -;
 DR EMBL; AF196571; AAF05834.1; -;
 DR EMBL; AF22310; AAG09716.1; -;
 DR EMBL; AV358892; AAO89251.1; -;
 DR EMBL; AL078605; CAB89569.1; -;
 DR HSSP; P00740; IEDM.
 DR Genew; HGNC:2908; DLL1.
 DR MIM; 606582; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005112; F:Notch binding; IPI.
 DR GO; GO:0030154; P:cell differentiation; TAS.
 DR GO; GO:0001709; P:cell fate determination; NAS.
 DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
 DR GO; GO:0009912; P:hair cell fate commitment; ISS.
 DR GO; GO:0030097; P:hemopoiesis; NAS.
 DR GO; GO:0042472; P:inner ear morphogenesis; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR GO; GO:0007219; P:Notch signaling pathway; NAS.
 DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
 DR GO; GO:0030155; P:regulation of cell adhesion; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR001774; DSL.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01414; DSL; 1.
 DR Pfam; PF00008; EGF; 6.
 DR PRINTS; PRO0010; EGFBLDOD.
 DR SMART; SM00051; DSL; 1.
 DR SMART; SM00179; EGF_Ca; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 8.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS00026; EGF_3; 7.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 723 Delta-like protein 1.
 FT DOMAIN 18 545 Extracellular (Potential).
 FT TRANSMEM 546 568 Potential.
 FT DOMAIN 569 723 Cytoplasmic (Potential).
 FT DOMAIN 159 221 DSL.
 FT DOMAIN 159 221 DSL.
 FT DOMAIN 226 254 EGF-like 1.
 FT DOMAIN 226 254 EGF-like 2.
 FT DOMAIN 257 285 EGF-like 3.
 FT DOMAIN 292 325 EGF-like 4.
 FT DOMAIN 332 363 EGF-like 5.
 FT DOMAIN 370 402 EGF-like 6.
 FT DOMAIN 409 440 EGF-like 7.
 FT DOMAIN 447 478 EGF-like 8.
 FT DOMAIN 485 516 EGF-like 9.
 FT DISULFID 226 237 By similarity.
 FT DISULFID 230 243 By similarity.
 FT DISULFID 245 254 By similarity.
 FT DISULFID 257 268 By similarity.
 FT DISULFID 263 274 By similarity.

FT DISULFID 276 285 By similarity.
 FT DISULFID 292 304 By similarity.
 FT DISULFID 298 314 By similarity.
 FT DISULFID 316 325 By similarity.
 FT DISULFID 332 343 By similarity.
 FT DISULFID 337 352 By similarity.
 FT DISULFID 354 363 By similarity.
 FT DISULFID 370 381 By similarity.
 FT DISULFID 375 391 By similarity.
 FT DISULFID 393 402 By similarity.
 FT DISULFID 409 420 By similarity.
 FT DISULFID 414 429 By similarity.
 FT DISULFID 431 440 By similarity.
 FT DISULFID 447 467 By similarity.
 FT DISULFID 469 478 By similarity.
 FT DISULFID 485 496 By similarity.
 FT DISULFID 490 505 By similarity.
 FT DISULFID 507 516 By similarity.
 FT CARBOHYD 477 477 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 498 498 E -> Q (in Ref. 2).
 FT CONFLICT 502 502 G -> R (in Ref. 4 and 5).
 FT CONFLICT 510 510 G -> S (in Ref. 2).
 SQ SEQUENCE 723 AA; 77956 MW; B4EC455FFA32A12B CRC64;
 Query Match 71.0%; Score 2401.5; DB 1; Length 723;
 Best Local Similarity 75.1%; Pred. No. 1.8e-167; Indels 139; Gaps 67;
 Matches 534; Conservative 11; Mismatches 27;
 QY 7 SALLC---VSGVFELKLOEFVNKGLL-NRNCRCGG-----GCCTFFRVCLKHQOASVS 56
 DB 13 SALLCQVWSSGVFELKLOEFVNKGLLNRNCRCGGAGPPPCACRTFFRVCLKHQOASVS 72
 QY 57 PEPPCTYQSA-TPVLG--SFS-PDAG-DPAFNSIRPPPGTWGTFSLIIEALHTDSP 111
 DB 73 PEPPCTYGSAPVPLGVDSFSLPDGGADSAFSPNIRFPFGFTWFGTFLSIIIEALHTDSP 132
 QY 112 DDL-TENPERLSRL-TORHL-VGEWSDLHSSGRTDL-VSYRPFVCDHHYVGECSVFC 167
 DB 133 DDLATENPERLSRLATQRHLTVGEWSDLHSSGRTDLKYRPFVCDHHYVGECSVFC 192
 QY 168 RPRDD-FGHFTCG-RGEK-C-PGWGQYCT-PICLPGCD-QHG-CDKPECKRCRVGQGR 220
 DB 193 RPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQHGFCDKPECKRCRVGQGR 252
 QY 221 YDECI RYPGCVHGTQQPWCNCGEGWGLFCNODLNYCTHHKPC-NGATCTNTQGSY 279
 DB 253 YDECI RYPGCLHGTQQPWCNCGEGWGLFCNODLNYCTHHKPCNGATCTNTQGSY 312
 QY 280 TCSRPYGTG--CE---BEC---PCKN-GSCDTLES--SCTCPGFGYK-CELSAMTCD 327
 DB 313 TCSRPYGTGATCELGIDECDDSPCKNGSGCTDLENSYCTCPGFGYKICELSAMTCD 372
 QY 328 GPCFNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYS-C-CQ 376
 DB 373 GPCFNGRCSDSPDGGYSRCPCPVYSGFNCEKKIDYCSSSPCSNAGAKVDLDGAYLCRCQ 432
 QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPGY-GKNCS-PVSCEH-PCNH 425
 DB 433 AGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPGFGYGRNCSAPVSCEHAPCHN 492
 QY 426 GATCHRR---YCECA-GYGG-NCQFLLEP-PPGP--VD-----BEQ---FPW-AVCAGL 467
 DB 493 GATCHERGHVYCECARGYGGNCFLLPELPPGAVVDLTKELGQGGGPPFWAVCAGV 552
 QY 468 VI---LLLGCAA-VVVCRL---KQPEC-----ETETMNNLANCQREK---SSIGATQI 512
 DB 553 ILVLMALLGCAAVVVCVRLRLQKRRPADPCRGETETMNNLANCQREKDISVSIIGATQI 612
 QY 513 KVTNKK-DPH-----DK---KVRYP-VDYNYL-----LKVHKC-----S 542
 DB 613 KVTNKADPHGDHSDAKNGFKARYPAVDYNYLVQDLKGGDTAVRDAHSKRDITKCPQGGSSG 672
 QY 543 BEKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578

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Db 673 BEKTPPTLRGGEASERKRPDGGCSTKDTKYQSYVYVISEKDEKCVIATEV 723
|||||
RESULT 9
Q8AW87 PRELIMINARY; PRT; 726 AA.
ID Q8AW87
AC Q8AW87
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ligand Delta-1.
GN Name=Delta-1.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; AB095017; BAC41350.2; -.
DR HSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL_1.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 726 AA; 79866 MW; 352A40219AE67F41 CRC64;

Query Match 67.0%; Score 2267.5; DB 2; Length 726;
Best Local Similarity 68.9%; Pred. No. 1.2e-157;
Matches 496; Conservative 23; Mismatches 56; Indels 145; Gaps 58;

Qy 4 LLASALICV-----SGVFELKIOEFYNNKGLL-NRNCRRGG-----CCTFFR 45
Db 7 LACAAALICVLCQVSCSGVFELKIOEFYNNKGLNANCCRAGSVQGALLQCCOCTFFR 66
Qy 46 VCLKHYQASVSPPCCTYGA-TPVL--GSFSPDGDGDPAFSNIPRPPFGTWPGETSLI 102
Db 67 VCLKHYQANVSPPCCTYGSANVPLVQGSFTYPEGGEATFNPIRATGFTWPGTFSLI 126
Qy 103 IEALHTDSPDL-TENPERLISRLT-QRHL-VGEWSDQLHSGRTDL-YSYRFVCDHY 158
Db 127 IGALHTDSPDLSTENPDRLISRMALQRHLAVGDSQDSQSSGRTDLKYSYRFVCDHY 186
Qy 159 YGEGCSVFCPRPD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC 211
Db 187 YGEGCSVFCPRPDFTFGHFTCGEGEKQCNQGWKGQYCTEAILCPGCDQHGFCDFRPEC 246
Qy 212 KCRVWGGRYCDCEIRYPGCVHGTCCQPPWCNQCQEGWGLFCNQDNLNCTHHKPC-NGAT 270
Db 247 KCRVWGGRYCDCEIRYPGCLHGTCCQPPWCNQCQEGWGLFCNQDNLNCTHHKPCNNAAT 306
Qy 271 CTNTGGSYTCSCRPGYTG--CE----BEC---PCKN-GSCTDLSES--SCTCPGFGYK-C 318
|||||
307 CTNTGGSYTCSCRPGYTGANCEIENVECEASPCCKNGSGCADLNSYSKSCPPGFGKNC 366
Qy 319 ELSAMTCADGCPFNNGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSS-PC-NGA-CVDL 369
Db 367 ELSAMTCADGCPFNNGRCSDNPEGGYSCRPLSYSGFNCEKKIDYCSNPNCSGAHCVDL 426
Qy 370 GNSYCCQA--GF-C-DNVDCAS-PC-NGGTC--VND-SCTCPGGY-GKNC-S-PVS 417
Db 427 GNSYICQLDGFSGRHCDDNLDCCASYPCANGGTCQDGVNDYSCTCPGNGKNCSTPVS 486
Qy 418 RCEH-PCNGATCHRR-----YCECA-GYGG-NCQFLPPEPPGPVDE-----EQ 458
Db 487 RCEHSPCHNGATCHERNRYVCECARGYGGLNCQFLPPEQFQEHDTGDNTEKYTEDQGGQ 546
Qy 459 FPW-AVCAGLVL---LLGCAA-VVCVRLKQKPE-----CETMTNNLANCOREKD 504
Db 547 FPWIAVCAGIILVLMLLFGCAAVVVCFRLKHKHQQRQSDSYSGESSETMNNLANCRREKD 606
Qy 505 ---SSIGATQIKNTNKK-----DFHDKKVRYP-VDYNLVL-----KVH 538
Db 607 ISVSVIGATQIKNTNKKADLYSESTSDKNGYKARYPSVDYNLVHELKHEDSVKEEHGKRE 666
Qy 539 KKC-----SEKALRKRP-SVYSTSKDTKYQSYV--SEKDEC-IATEV 578
Db 667 SKCIANGSEADEKHPVLKSSSETSERRPESLYSTSKETKYQSYVYVISEANDECIATEV 726

RESULT 10
Q91902 PRELIMINARY; PRT; 721 AA.
ID Q91902
AC Q91902;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE X-Delta-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319507; PubMed=7596411;
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the
RT chick.";
RL Nature 375:787-790 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319503; PubMed=7596407;
RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
RT "Primary neurogenesis in Xenopus embryos regulated by a homologue of
RT the Drosophila neurogenic gene Delta.";
RL Nature 375:761-766 (1995).
DR EMBL; L42229; AAC38017.1; -.
DR HSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.

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QY 503 KD-----SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVKLVHK-----539
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 KDLVSIIGATQVKNINKKVDQSDGKNGKFSYSLVDYNLVHKLQEDLGKEDSRSE 660

QY 540 --KC-----SEEK-----ALRKPSVYSTSKTKYQSVVY--SEKDEC-IATEV 578
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 ATKCEPLDSDSEKHNLKSDSERKRT--SLCKDTKYQSVFVLSEKDECIATEI 717

RESULT 12
P87357
ID P87357 PRELIMINARY; PRT; 717 AA.
AC P87357;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DeltaD transmembrane protein precursor.
GN Name=dlD; Synonyms=deltaD;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97346722; PubMed=9203139;
RA Dornseifer P., Takke C., Campos-Ortega J.A.;
RT "Overexpression of a zebrafish homologue of the Drosophila neurogenic
RT gene delta perturbs differentiation of primary neurons and somitic
RT development.";
RL Mech. Dev. 63:159-171(1997).
DR EMBL; Y11760; CAA72425.1; -.
DR HSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-990415-47; dld.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005009; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM0051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain; Signal; Transmembrane.
FT SIGNAL 4 11 Potential.
SQ SEQUENCE 717 AA; 79601 MW; 9C5A0162504593B4 CRC64;

Query Match 61.58; Score 2081.5; DB 2; Length 717;
Best Local Similarity 63.48; Pred. No. 5e-144;
Matches 456; Conservative 51; Mismatches 69; Indels 143; Gaps 59;

QY 1 MGRLLASALLCV-----SGVFELKQEFVNKKGLL-NRNCRCGGG-----CCTFFR 45
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MGRLLMIAVLVCWISQFCGSGVFELKQEFVNKKGLLGNVGNANCKGSAEGHQCEKTFPR 60

QY 46 VCLKHQASVSPPECTYGA-TPVLGFS---PDGAGDPAFNSPIRPFPGFTWPGTFL 101
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 ICLKHQANVSPDPCCTYGAVTPVLGNSGFQVPSFDSFTNPIPFAGFTWPGTFL 120

QY 102 IIEALHTDSDDDL-TENPERLISRL-TQRHL-VGEESWQDLHSSGRDIL-YSTRFVCD 157
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 IIEALHTDSDDDLSTENPDRLISMTTQRHLTVGEESWQDLQVGRTELKYSRVCDEH 180

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QY 158 YYEGSCSVFRPRDD-FGHFTCG-RGE-KC-PGWKGQYCT-PICLPQCDQ-HG-CDKPG 210
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 YYEGSCSVFRPRDDTGHFTCGERGEIICNSGKQYCTEPICLPGCDEDHGFCDFKPG 240

QY 211 CKRNVGHQGRYCBECIRYPCVHGTCTQPCQNCQCBGGLFCNQDLNYCTHHKPC-NGA 269
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 CKRVGSGRYCDDCIRYPQCLHGTCTQPCQNCQCBGGLFCNQDLNYCTHHKPCQNGA 300

QY 270 TCTNTGSGYSTCSCRPGVTG-CB---EBC---PCKN-GSCTDLES--SCTCPGFGYK- 317
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 TCTNTGSGYSTCSCRPGFTGDSCEIEVNEGSGSPCRNGSGCTDLENYCTCPGFGYGRN 360

QY 318 CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEBK--DCSS-PC--NGACVD 368
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 CELSAMTCADGPCFNGGHCADNPEGGYFCPCPMYAGFNCEKKIDHCSSNFCSDAQCCLD 420

QY 369 LGNSYCCQAGFG----RC-DNVDCCAS-PC-NGGTCD--VND-SCTCPGGY-GKNC-SPV 416
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 LVDSYLCQCPGFTGTHTCEDNIDECATYPCQNGGTCTQDGLSDYCTCTCPGGYTGKNTSAV 480

QY 417 SRCEH-PCNMGATCH---BRYCEB-AGYGC-NCOFLPE-PPGPV-----D 455
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 NKCLNPNCHMGATCHENDNRVVCATPGYGRNCOFLPENPQQAIVEGADKRYSEED 540

QY 456 EEQFPW-AVCAGLVLLLL-----GCAAVVCVRLKQK-----PECETETNNLANCO-RE 502
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 DGGFPWTAVCAGIILVLLVLLGSGVFYIYIRLKLQORSQQIDSHSEIETNNLTNRSRE 600

QY 503 KD---SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVKLVHK-----539
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 KDLVSIIGATQVKNINKKVDQSDGKNGKFSYSLVDYNLVHKLQEDLGKEDSRSE 660

QY 540 --KC-----SEEK-----ALRKPSVYSTSKTKYQSVVY--SEKDEC-IATEV 578
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 ATKCEPLDSDSEKHNLKSDSERKRT--SLCKDTKYQSVFVLSEKDECIATEV 717

RESULT 13
Q6DI48
ID Q6DI48 PRELIMINARY; PRT; 772 AA.
AC Q6DI48;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Spatleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallos D.E., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences. ";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075742; AAH75742.1; -.
KW Hypothetical protein.
SQ SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;

Query Match          59.5%; Score 2014; DB 2; Length 772;
Best Local Similarity 58.4%; Pred. No. 4.8e-139;
Matches 452; Conservative 48; Mismatches 76; Indels 198; Gaps 61;

QY 1 MGR-----LLAS---ALLC---VSGVFELKQBFVNKKGLL-NRNCRRG-----GCC 41
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MGRHULLLLFSILYMLLCQASSSGVFELKQBFVNKKGVQGNKCKGGLTTSYQOCECK 60
QY 42 TFFRVCLKHQYQASVSPPEPCTY-GSATPVLSGFS---PDGADPAFSPNPIRPFPGFTWPG 97
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 TFFRICLKHQYQNASPEPCTYGGTVPVLGNSFQVPTLPGSGFTNPIRNFPGFTWPG 120
QY 98 TFSLIIEALHTSPDDL-TENPERLISRL-TORHL-VGEWSDQLHSSGRTDL-YSYREV 153
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 TFSLIIEALHADSKEDELTENPERIISTMTTORHLTVGEDNSQDLHSVGRTELKYSYREV 180
QY 154 CDEHYVGGSCVFCRPRDD-FGHFTCG-RGE-KC-PGWKGYCT-PICLPQGD-QHG-CD 206
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 CDEHYVGGSCVFCRPRDDAFGHFTCGERGEIICDAGWKGYCTBPICLPQGDDEHGFC 240
QY 207 KPGECKRCVWGQRYCDEIRPGCVHGTCCQPWQCNCOEGWGLFCNODLNYCTHHKPC 266
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 KPGECKRCVGFGRYDEGIRYPCGLHGTCCQPWQCNCOEGWGLFCNODLNYCTHHKPC 300
QY 267 -NGATCTNTGQSYTCSCRPGVTG--CE---EBC---PCKN-GSCTDLES---SCTCPGPF 314
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 LNGATCSNTGQSYTCSCRPGFSGASCEIEVNECTGNPCRNCGSCTDMENTYCTCPGPF 360
QY 315 YGK-CELSAMTCADGCFNCGRC-DNPDGGY-C-CPLG-SGFNCKEKK--DC-SSPC-NGA 365
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 YGKNCCELSAMTCADGCFNCGRCADNPDDGGYFCQCPGVAGFNCKEKKIDHCSSPCNCA 420
QY 366 -CVDLGNVSCCQAGFG----RCDNV-DDCAS-PC-NGTCDVNS---CTCPGY-GRNC 413
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 RCVDLNVSLYCCQPDGFTGMCDRAGDECSYPCQNGGTCCBGASGYMCTCPGYTGRC 480
QY 414 -SPVSRCEH-PCHNGATCHRR---YCEG-AGYGG-NCQFLPPEPPGVDEQFPW-AVC 464
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 481 SSFVSRQHPCHNGATCHERNRNVYACVSGYGRNCOFLPDRASQIASD-VPWTAVG 539
QY 465 AGLVLLLL---GCA-AVVCRLK-----QKPECETETMNNLA-NCQREK---SS 506
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 540 SGVLLVLLLVACAVVVCVRSKVQRRDRREDEVANGENETINLTNNCHRDKDLAVSV 599
QY 507 IGATQIKNTKK-DP---HDK-----KVRY-PVDYNYL-----534
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 600 VGVAPVKNINKIDFSDHDDLSLTTEKRSYKTRHAPADYNLVHEVFEVGEVKLEHAG 659
QY 535 -----LKVHKKCSBEKALRKR-----PS 552
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 660 KETTWANELSDCEDIKQCSLQDSSECTEKR-RKRLKSDASEKYSYRSYSEKYS 718
QY 553 VYSTK-----DTKYQSVVY--SEKDEC-IATEV 578
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 719 KYSEKYSVSLVSESACASACASASTSACVDTKYKSVVMSEKDECVIATEV 772

RESULT 14
O57462
ID O57462
AC O57462;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
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